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result set

DB=PGPB,DWPI; PLUR=YES; OP=OR

<u>L8</u>	L7 and humanized	49	<u>L8</u>
<u>L7</u>	L6 and antibody	118	<u>L7</u>
<u>L6</u>	IL-18 or IGIF or interleukin-18 or (interferon adj3 inducing adj1 factor) or (interferon-gamma adj1 inducing adj1 factor)or IL18	155	<u>L6</u>

DB=USPT; PLUR=YES; OP=OR

<u>L5</u>	Okamura-Haruki.in. or Okura-Takanori.in. or Torigoe-Kakuji.in. or Ushio-Shimpei.in.	31	<u>L5</u>
<u>L4</u>	Okamura-Haruki.in. or Okura-Takanori.in.	28	<u>L4</u>
<u>L3</u>	L1 and antibody.clm.	24	<u>L3</u>
<u>L2</u>	L1 and antibody	100	<u>L2</u>
<u>L1</u>	IL-18 or IGIF or interleukin-18 or (interferon adj3 inducing adj1 factor) or (interferon-gamma adj1 inducing adj1 factor)or IL18	109	<u>L1</u>



65379

Delaval, Jan

From: Roark, Jessica
Sent: Friday, June 21, 2002 7:48 AM
To: Delaval, Jan
Subject: 09/780035

Jan,

I have to extend a search to other species of the invention.

Please search, including pending, for the following from 09/780,035:

All sequences open only, unless otherwise noted.

SEQ ID NO:61
SEQ ID NO:3, closed only (this is a subsequence of SEQ 61)
SEQ ID NO:33, closed only (this is a subsequence of SEQ 61)

SEQ ID NO:18
SEQ ID NO:19

SEQ ID NO:28
SEQ ID NO:28 from 21-25
SEQ ID NO:28 from 40-56
SEQ ID NO:28 from 89-97

SEQ ID NO:29
SEQ ID NO:29 from 23-35
SEQ ID NO:29 from 51-57
SEQ ID NO:29 from 90-100.

Results on paper please.

Thanks!

Jessica H. Roark

CM1 9D04
Mailbox 9E12
Art Unit 1644
703 605-1209

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:18 ; Search time 245.49 Seconds
(without alignments)
71.036 Million cell updates/sec

Title: US-09-780-035-61

Perfect score: 816
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKEDLDGDSIMFTWQNEED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802:*

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- 3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
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- 6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
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- 13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
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- 19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	816	100.0	157	19	AAW77077
2	816	100.0	157	22	AAW57570
3	816	100.0	157	22	AAE06661
4	816	100.0	157	22	AAE065294
5	816	100.0	157	22	AAE065351
6	816	100.0	158	21	AAE85167
7	816	100.0	180	19	AAW48959
8	816	100.0	193	18	AAW22047
9	816	100.0	193	18	AAW46592
10	816	100.0	193	22	AAE30541
11	816	100.0	193	22	AAE65830

12	813	99.6	193	19	AAW77082	Interleukin 18 act
13	811	99.4	157	17	AAE99564	Human interleukin-g
14	811	99.4	157	17	AAE99558	Human mature inter
15	811	99.4	157	18	AAW15701	Interleukin-gamma 1
16	811	99.4	157	18	AAW24258	Human protein for
17	811	99.4	157	19	AAW77158	Human interleukin-
18	811	99.4	157	19	AAW63810	Human IL-18 protel
19	811	99.4	157	19	AAW37741	IFN-gamma inducing
20	811	99.4	157	19	AAW52176	Interleukin-gamma 1
21	811	99.4	157	20	AAW39799	Interleukin-18 rec
22	811	99.4	157	21	AAW44597	Human interleukin-
23	811	99.4	157	21	AAW53904	Sequence of a matu
24	811	99.4	157	22	AAE82408	Human interleukin-
25	811	99.4	193	17	AAE99560	Human interleukin-g
26	811	99.4	193	19	AAW37740	Interleukin-gamma 1
27	811	99.4	193	19	AAW52172	Interleukin-gamma 1
28	811	99.4	193	19	AAW47429	Interleukin-gamma p
29	811	99.4	193	21	AAW53908	Amino acid sequenc
30	811	99.4	193	22	AAE82409	Human interleukin-
31	808	99.0	193	22	AAW31757	Interleukin-gamma 1
32	806	98.8	157	19	AAW77083	Human interleukin
33	806	98.8	157	19	AAW48961	Mutant human inter
34	806	98.8	181	21	AAE23797	Macaca cynomolgus
35	797	97.7	193	22	AAW72608	Human interleukin
36	796	97.5	157	19	AAW77084	Human interleukin
37	796	97.5	157	19	AAW77085	Human interleukin
38	796	97.5	157	19	AAW48962	Mutant human inter
39	796	97.5	157	19	AAW48963	Mutant human inter
40	787	96.4	157	19	AAW77080	Human interleukin
41	787	96.4	157	19	AAW77088	Human interleukin
42	787	96.4	157	19	AAW48966	Mutant human inter
43	786	96.3	157	19	AAW77086	Human interleukin
44	786	96.3	157	19	AAW48964	Mutant human inter
45	777	95.2	157	19	AAW77081	Human interleukin

ALIGNMENTS

RESULT 1	AAW77077	standard; peptide; 157 AA.
ID	AAW77077	
XX	AAW77077;	
AC	16-NOV-1998 (first entry)	
XX	Human interleukin 18.	
DE	Human: interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;	
KW	osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;	
KW	chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.	
XX		
OS	Homo sapiens.	
XX	EP861663-A2.	
PN	02-SEP-1998.	
XX		
PD	24-FEB-1998; 98EP-0301352.	
XX		
PR	25-FEB-1997; 97JP-0055468.	
XX		
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.	
XX		
PI	Gillespie MT, HORWOOD NJ, Kurimoto M, Udagawa N;	
DR	WPI: 1998-448964/39.	
XX	N-PSDB: AAV48226.	
PT	Use of interleukin-18 to inhibit osteoclast formation - in treatment	
PT	of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,	
PT	osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,	

PT primary hyperthyroidism and osteoporosis
 XX
 XX Claim 4; Page 18; 56pp; English.
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SQ Sequence 157 AA;
 Query Match 100.0%; Score 816; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDGNNRPLFEDMTDSDCRDNPRTIFISMYKDSQPRGM 60
 DB 1 yfgklesklsvirnlndqvlfdggnrplfedmtsdcdndaprtiflismykdsqprgm 60
 QY 61 AVTISVKCEKISTLSCENKIIISFKENPPDNKIKDTSIIFFORSVPGHDKMQFESSSY 120
 DB 61 avtiskcekistlscenkliisfkemppdnkikdtsdiiifforsvpgdhkmqfesssy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 157
 DB 121 egyflacekerdlfkilkkedelgdrsimftvgned 157
 RESULT 2
 AAY57570
 ID AAY57570 standard; Protein; 157 AA.
 AC AAY57570;
 XX
 DT 06-MAR-2000 (first entry)
 XX
 DE Human Interleukin 18 protein sequence SEQ ID NO:1.
 XX
 KW Human; Interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;
 KW interferon-gamma-inducing factor; growth inhibition; cytostatic.
 OS Homo sapiens.
 XX
 PN WO959565-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-US11160.
 XX
 PR 21-MAY-1998; 98US-0086560.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Johnson RK;
 XX
 DR WPI; 2000-062368/05.
 XX
 PT New polypeptides, useful for preparation of composition for preventing
 PT and/or treating cancer by inhibiting tumor growth
 XX
 XX Claim 1; Page 49-50; 53pp; English.
 CC The present sequence represents human interleukin 18 (IL-18). The
 CC present invention describes a compound comprising human or murine IL-18
 CC in combination with a chemotherapeutic agent (I). Also described are:
 CC (1) a method of preventing and/or treating cancer in a mammal comprising
 CC the administration of a cancer inhibiting amount of (I) comprising the
 CC IL-18 protein and the chemotherapeutic agent and optionally a
 CC pharmaceutically acceptable carrier; and (2) a method of inhibiting the
 CC growth of tumour cells in a mammal sensitive to a composition comprising

CC human IL-18 and/or murine IL-18 and the chemotherapeutic agent (and
 CC optionally a pharmaceutically acceptable carrier), comprising
 CC administering to a mammal afflicted with the tumour cells an effective
 CC tumour cell growth inhibiting amount of (I). The IL-18 protein in
 CC conjunction with a chemotherapeutic agent is useful in a method for
 CC preventing and/or treating cancer in mammals by inhibiting the growth
 CC of tumours or cancerous cells in mammals.
 XX
 SQ Sequence 157 AA;
 Query Match 100.0%; Score 816; DB 21; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDGNNRPLFEDMTDSDCRDNPRTIFISMYKDSQPRGM 60
 DB 1 yfgklesklsvirnlndqvlfdggnrplfedmtsdcdndaprtiflismykdsqprgm 60
 QY 61 AVTISVKCEKISTLSCENKIIISFKENPPDNKIKDTSIIFFORSVPGHDKMQFESSSY 120
 DB 61 avtiskcekistlscenkliisfkemppdnkikdtsdiiifforsvpgdhkmqfesssy 120
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 157
 DB 121 egyflacekerdlfkilkkedelgdrsimftvgned 157
 RESULT 3
 AAE06661
 ID AAE06661 standard; Protein; 157 AA.
 AC AAE06661;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human interleukin-1gamma (IL-1gamma) protein.
 XX
 KW Human; Interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;
 KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
 KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
 KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
 OS Homo sapiens.
 XX
 PN WO200157219-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 01-FEB-2001; 2001WO-US03285.
 XX
 PR 02-FEB-2000; 2000US-0179638.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
 XX
 DR WPI; 2001-488886/53.
 XX
 PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
 PT polypeptide useful for treating conditions exhibiting abnormal
 PT expression of interleukin such as immunological disorders, tumor and
 PT allergy
 XX
 XX Disclosure; Fig 1; 103pp; English.
 CC The invention relates to recombinant antigenic interleukin-1 like
 CC molecules and their corresponding nucleic acid sequences, designated
 CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
 CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
 CC abnormal expression of the interleukin such as immunological disorders,
 CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary

CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC HIV). The invention also relates to methods of using the composition
CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC utilities. IL-1delta is used as an immunogen for the production of
CC antisera or antibodies specific, e.g., capable of distinguishing between
CC IL-1 family members and an IL-1delta, for the interleukin or its
CC fragment. The purified interleukin is used as a reagent to detect any
CC antibodies generated in response to the presence of elevated levels of
CC expression, or immunological disorders which lead to antibody production
CC to the endogenous cytokine. The invention also contemplates the use of
CC competitive drug screening assays. The present sequence is human
CC interleukin-1gamma (IL-1gamma) protein related to the invention.

SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 22; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDVLFIDGKRPFLFEDMTSDCDRNAPRTTIFISMYKDSQPRGM 60
|
| 1 yfgklesklsvirnlndvlfidgknpflfedmtsdcdrdnaprtlffismykdsqprgm 60
|
QY 61 AVTISVCKEISTLSCENKTIISFKEMNPPDNIKDTKSDIIFPQSRVPGHDNKKQFESSY 120
|
| 61 avtisivckeistlscenkktisfkemnpdpnldktsdliifqsrvgpndnkmqfessy 120
|
DB 61 AVTISVCKEISTLSCENKTIISFKEMNPPDNIKDTKSDIIFPQSRVPGHDNKKQFESSY 120
|
| 61 avtisivckeistlscenkktisfkemnpdpnldktsdliifqsrvgpndnkmqfessy 120
|
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEQ 157
|
| 121 egyflacekerdlfkllkkelldgtrsimftvqned 157
|

RESULT 4

AAG65294 standard; protein; 157 AA.

AAG65294;

30-NOV-2001 (first entry)

Human Interleukin-18 (IL-18) protein fragment.

IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.

Homo sapiens.

WO200158956-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US04170.

10-FEB-2000; 2000US-0181608.

(BADI) BASF AG.

PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfield J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
DR WPI; 2001-550020/61.

Novel antibodies and compounds capable of binding to human
interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

Disclosure; Page 9; 91pp; English.

The invention provides isolated antibodies, or antigen-binding portions,

CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents a human IL-18 protein fragment.

SQ Sequence 157 AA;

Query Match 100.0%; Score 816; DB 22; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDVLFIDGKRPFLFEDMTSDCDRNAPRTTIFISMYKDSQPRGM 60
|
| 1 yfgklesklsvirnlndvlfidgknpflfedmtsdcdrdnaprtlffismykdsqprgm 60
|
QY 61 AVTISVCKEISTLSCENKTIISFKEMNPPDNIKDTKSDIIFPQSRVPGHDNKKQFESSY 120
|
| 61 avtisivckeistlscenkktisfkemnpdpnldktsdliifqsrvgpndnkmqfessy 120
|
DB 61 AVTISVCKEISTLSCENKTIISFKEMNPPDNIKDTKSDIIFPQSRVPGHDNKKQFESSY 120
|
| 61 avtisivckeistlscenkktisfkemnpdpnldktsdliifqsrvgpndnkmqfessy 120
|
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEQ 157
|
| 121 egyflacekerdlfkllkkelldgtrsimftvqned 157
|

RESULT 5

AAG65351 standard; protein; 157 AA.

AAG65351;

30-NOV-2001 (first entry)

Human Interleukin-18 (IL-18) protein fragment.

IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.

Homo sapiens.

WO200158956-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US04170.

10-FEB-2000; 2000US-0181608.

(BADI) BASF AG.

PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfield J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SN;
DR WPI; 2001-550020/61.

Novel antibodies and compounds capable of binding to human
interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

Disclosure; Page 14; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 protein fragment.
 XX
 SQ Sequence 157 AA:
 Query Match 100.0%; Score 816; DB 22; Length 157;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 60
 QY 61 AVTISVCKEKISTLSCENKISFKEMNPDPNIDKTSIDIFFORSVPGHDKMKOFESSSY 120
 DB 61 AVTISVCKEKISTLSCENKISFKEMNPDPNIDKTSIDIFFORSVPGHDKMKOFESSSY 120
 QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
 DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
 RESULT 6
 AAY85167
 ID AAY85167 standard; Protein; 158 AA.
 XX
 AC AAY85167;
 XX
 DT 23-JUN-2000 (first entry)
 XX
 DE Human interleukin-18 (IL-18) amino acid sequence.
 XX
 KW Interleukin-18; production; IL-18; human; medical injection product.
 XX
 OS Homo sapiens.
 XX
 PN CN1243130-A.
 XX
 PD 02-FEB-2000.
 XX
 PF 24-JUL-1998; 98CN-0103307.
 XX
 PR 24-JUL-1998; 98CN-0103307.
 XX
 PA (WUGG/) WU G.
 XX
 PI Wu G, Liu Z;
 XX
 DR WPI; 2000-340020/30.
 DR N-PSDB; AAA10526.
 XX
 PT Preparation method for engineering bacteria for recombination of human
 PT Interleukin-18 and its product thereof -
 XX
 PS Claim 1; Page 2; 17pp; English.
 XX
 CC This sequence represents the human interleukin-18 (IL-18) amino acid
 CC sequence. The invention relates to a method for engineering bacterium for

CC recombination of human IL-18 and a method for the preparation of IL-18. A
 CC primer containing a restriction endonuclease site can be used to
 CC accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
 CC stop codon preferred by coli bacillus to raise the expression rate. The
 CC method uses a high-amplification culture medium to increase the
 CC expression level and only requires a one-step purification process to
 CC obtain a medical injection-pure product.
 XX
 SQ Sequence 158 AA:
 Query Match 100.0%; Score 816; DB 21; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.2e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 60
 DB 2 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDRNAPRTFIISMYKDSQPRGM 61
 QY 61 AVTISVCKEKISTLSCENKISFKEMNPDPNIDKTSIDIFFORSVPGHDKMKOFESSSY 120
 DB 62 AVTISVCKEKISTLSCENKISFKEMNPDPNIDKTSIDIFFORSVPGHDKMKOFESSSY 121
 QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
 DB 122 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 158
 RESULT 7
 AAW48959
 ID AAW48959 standard; Peptide; 180 AA.
 XX
 AC AAW48959;
 XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Wild-type human interferon-gamma inducing factor.
 XX
 KW Interferon-gamma inducing factor; Interferon-gamma; Killer cell;
 KW antitumor agent; antiviral agent; antimicrobial agent; tumour; IGF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..23
 FT /note= "Signal peptide"
 FT Protein 24..180
 FT /note= "Mature human IGF which is claimed by the
 FT Inventors under claim 3 in the specification"
 XX
 PN EP845530-A2.
 XX
 PD 03-JUN-1998.
 XX
 PF 28-NOV-1997; 97EP-0309632.
 XX
 PR 14-NOV-1997; 97JP-0329715.
 PR 29-NOV-1996; 96JP-033037.
 PR 21-JAN-1997; 97JP-0020906.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Kurimoto M, Okamoto I, Yamamoto K;
 XX
 DR WPI; 1998-286747/26.
 DR N-PSDB; AAV32754.
 XX
 PT Mutants of interferon-gamma inducing polypeptide - useful as
 PT antitumour, antiviral, antimicrobial or anti-immunopathic agents
 XX
 PS Claim 3; pages 36-37; 59pp; English.

XX The present sequence represents the wild-type human interferon-gamma
 CC inducing factor (IGIF). The invention provides for mutant human and
 CC mouse interferon-gamma inducing factors in which one or more cysteine
 CC residues are replaced with different residues at or away from the
 CC consensus sequences shown in AAW48956-W48958. The mutant IGIFs are
 CC capable of stimulating immunocompetent cells for the production of
 CC interferon-gamma and are claimed to be less toxic, more active and
 CC stable than the corresponding wild type IGIF. The mutant IGIFs are also
 CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
 CC formation, and may therefore be useful as antitumour agents, antitumour
 CC immunotherapeutics, antiviral agents and antimicrobial agents. The
 CC mutant IGIFs are also claimed to be useful for treating hepatitis, solid
 CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
 CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
 CC thrombopenia caused by radiation- and chemo-therapy.

SQ Sequence 180 AA;

Query Match 100.0%; Score 816; DB 19; Length 180;
 Best Local Similarity 100.0%; Pred. No. 1.5e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YFGKLESKLSVIRNLDQVLFIDGNRPLEFDMTSDCRDNAPRTTITISMYKKSQPRGM 60
 |||||||
 DB 24 YFGKLESKLSVIRNLDQVLFIDGNRPLEFDMTSDCRDNAPRTTITISMYKKSQPRGM 83
 |||||||

OY 61 AVTISVKCEKISTLSCENKISTSFKEKMPNDIKDTSIIFFQRSVPGHDNKMFESSSY 120
 |||||||
 DB 84 AVTISVKCEKISTLSCENKISTSFKEKMPNDIKDTSIIFFQRSVPGHDNKMFESSSY 143
 |||||||

OY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYQNEED 157
 |||||||
 DB 144 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYQNEED 180
 |||||||

RESULT 8
 AAW22047
 ID AAW22047 standard; Protein; 193 AA.
 XX
 AC AAW22047;
 XX
 DT 14-JAN-1998 (first entry)
 XX
 DE Interferon gamma inducing factor-2 (IGIF-2) protein.
 XX
 KW Interferon gamma inducing factor-2; IGIF-2; leucocyte; lymphocyte;
 KW inflammation; proliferation; differentiation; maturation; tissue damage;
 KW human.
 KW
 XX Homo sapiens.
 OS
 OS
 PN W09724441-A1.
 XX
 PD 10-JUL-1997.
 XX
 PF 20-DEC-1996; 96WO-US20432.
 XX
 PR 29-DEC-1995; 95US-0580667.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Cocks BG, Coleman R, Hawkins PR;
 XX
 DR WPI: 1997-363677/33.
 DR N-PSDB; AAT74987.
 XX
 PT Novel interferon gamma inducing factor-2 - used to screen for
 PT compounds to diagnose, treat or prevent tissue damage associated
 PT with inflammation
 XX
 PS Claim 1; Page 46; 60pp; English.

XX This is the protein sequence of interferon gamma inducing factor-2
 CC (IGIF-2). An IGIF-2 variant (AAW31157) and an IGIF variant (AAW22049),
 CC which may be an alternate transcript, also exist. Probes derived from
 CC the nucleic acid sequences can be used to quantify the expression of
 CC IGIF-2 in conditions that are associated with inflammation or aberrant
 CC expression of IGIF-2. The protein can be used to screen for compounds
 CC that interact with IGIF-2, such as antibodies, antagonists or other
 CC inhibitors (especially ribozymes or antisense sequences) of IGIF-2
 CC expression or activity. The protein can also be used to diagnose,
 CC prevent or treat IGIF-2 induction of proliferation, differentiation or
 CC maturation of leucocytes or lymphocytes, especially in relation to tissue
 CC damage associated with inflammation.

SQ Sequence 193 AA;

Query Match 100.0%; Score 816; DB 18; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.6e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YFGKLESKLSVIRNLDQVLFIDGNRPLEFDMTSDCRDNAPRTTITISMYKKSQPRGM 60
 |||||||
 DB 37 YFGKLESKLSVIRNLDQVLFIDGNRPLEFDMTSDCRDNAPRTTITISMYKKSQPRGM 96
 |||||||

OY 61 AVTISVKCEKISTLSCENKISTSFKEKMPNDIKDTSIIFFQRSVPGHDNKMFESSSY 120
 |||||||
 DB 97 AVTISVKCEKISTLSCENKISTSFKEKMPNDIKDTSIIFFQRSVPGHDNKMFESSSY 156
 |||||||

OY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYQNEED 157
 |||||||
 DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYQNEED 193
 |||||||

RESULT 9
 AAW46592
 ID AAW46592 standard; Protein; 193 AA.
 XX
 AC AAW46592;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Amino acid sequence of human interleukin-1-gamma.
 XX
 KW Interleukin-1-gamma; IL-1-gamma; mouse; cytokine; IGIF; interferon-gamma;
 KW induction; antibody; diagnostic assay; fusion protein; activity;
 KW immunological disorder; allergy.
 KW
 XX Homo sapiens.
 OS
 OS
 FH Key
 FT Region
 FT Location/Qualifiers
 FT 41..47
 FT /note="beta-1 region"
 FT 55..59
 FT /note="beta-2 region"
 FT 64..68
 FT /note="beta-3 region"
 FT 83..88
 FT /note="beta-4 region"
 FT 96..102
 FT /note="beta-5 region"
 FT 108..113
 FT /note="beta-6 region"
 FT 115..120
 FT /note="beta-7 region"
 FT 137..143
 FT /note="beta-8 region"
 FT 147..153
 FT /note="beta-9 region"
 FT 160..164
 FT /note="beta-10 region"
 FT 170..175
 FT /note="beta-11 region"

FT Region 187..191
 FT /note="beta-12 region"
 XX
 PN WO9744468-A1.
 XX
 PD 27-NOV-1997.
 XX
 PF 16-MAY-1997; 97WO-US07282.
 XX
 PR 20-MAY-1996; 96US-0551998.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Bazan JF, Hardiman GT, Kastelein RA, Sana TR, Timans JC;
 XX
 DR WPI: 1998-018532/02.
 XX
 DR N-PSDB: AAV05368.
 XX
 PT Antagonist of human interleukin-1-gamma - used for treating
 PT Immunological disorders caused by human IL-1-gamma
 XX
 PS Disclosure: Pages 54-55; 63pp; English.
 XX
 CC The present sequence represents human interleukin-1-gamma (IL-1-gamma).
 CC The protein is the human equivalent of a mouse cytokine, IGIF, which
 CC induces certain T cells to produce interferon-gamma. Human IL-1-gamma
 CC and mouse IGIF show 71% identity at the nucleotide level and
 CC approximately 65% identity at the amino acid level. Antagonists of
 CC IL-1 gamma, e.g. antibodies, can be used in a method for treating a
 CC condition caused by human IL-1 gamma. The antibodies can also be used
 CC in diagnostic assays. The IL-1-gamma protein can be covalently
 CC conjugated to polyethylene glycol or to a polypeptide, and the fusion
 CC protein used in a pharmaceutical composition for supplying the
 CC biological activity of IL-1 gamma. Conditions that can be treated using
 CC the human IL-1 gamma protein include immunological disorders, allergies,
 CC and infectious diseases. The IL-1-gamma can also be used to detect the
 CC presence of the protein or its receptor.
 XX
 SQ Sequence 193 AA;

Query Match 100.0%; Score 816; DB 19; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1,6e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESLSVIRNLNDVLFIDQGNRPLEFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60
 DB 37 yfgkleskslvirnlndqvlfidggnrpifedmtsdcrdnaprtilfifismykdsgprgm 96
 QY 61 AVTISVCKEKTISLSCENKTIISFEKMNPPDNINKDKTSDIIFQRSVPGHDKMKQFESSSY 120
 DB 97 avtislvcckektislscenkktisfemnpdnlkdktsdliffqrsvpgdhnmqfesssy 156
 QY 121 EGYFLACEKERDLFKILIKKEDLGDRSIMFTYQNE 157
 DB 157 egyptlaccerkdlfkilikkedlgdrsimftvqned 193
 RESULT 10
 AAB30541
 ID AAB30541 standard; Protein; 193 AA.
 XX
 AC AAB30541;
 XX
 DT 06-MAR-2001 (first entry)
 XX
 DE A human IL-18 with a caspase-8 cleavage site.
 XX
 KW Protease cleavage site; caspase-1; interleukin-18; IL-18; protease.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Cleavage-site 33..36
 FT /note="caspase-8 cleavage site"
 XX
 XX WO200061768-A2.
 XX
 XX 19-OCT-2000.
 XX
 XX 13-APR-2000; 2000WO-IL00220.
 XX
 XX 13-APR-1999; 99IL-0129427.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Rubinstein M, Liu B, Novick D, Dinarello C, Graber P;
 XX
 DR WPI: 2001-006910/01.
 XX
 DR N-PSDB: AAC62200.
 XX
 PT Preparation of biologically active molecules from its inactive
 PT precursors, comprises mutating their native cleavage site to a site
 PT capable of being cleaved by protease and cleaving the mutated molecule
 XX
 PS Disclosure: Fig 8a-D; 40pp; English.
 XX
 CC The present sequence represents a human pro interleukin-18 (IL-18)
 CC with a caspase-8 cleavage site. The natural cleavage site of IL-18
 CC was mutated to a site susceptible to cleavage by a common protease.
 CC The specification describes a method for the preparation of biologically
 CC active molecules from their biologically inactive precursors. The method
 CC comprises mutating the native cleavage site to a site capable of being
 CC cleaved by a protease and cleaving the mutated molecule to yield the
 CC active compound. The method is especially used to produce active
 CC cytokines, such as IL-18.
 XX
 SQ Sequence 193 AA;

Query Match 100.0%; Score 816; DB 22; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1,6e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESLSVIRNLNDVLFIDQGNRPLEFEDMTDSDCRDNAPRTIFITISMYKDSQPRGM 60
 DB 37 yfgkleskslvirnlndqvlfidggnrpifedmtsdcrdnaprtilfifismykdsgprgm 96
 QY 61 AVTISVCKEKTISLSCENKTIISFEKMNPPDNINKDKTSDIIFQRSVPGHDKMKQFESSSY 120
 DB 97 avtislvcckektislscenkktisfemnpdnlkdktsdliffqrsvpgdhnmqfesssy 156
 QY 121 EGYFLACEKERDLFKILIKKEDLGDRSIMFTYQNE 157
 DB 157 egyptlaccerkdlfkilikkedlgdrsimftvqned 193
 RESULT 11
 AAG63830
 ID AAG63830 standard; Protein; 193 AA.
 XX
 AC AAG63830;
 XX
 DT 26-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of human interleukin 18 (IL-18).
 XX
 KW T-cell-helper type 2 response; Th2 response; T cell mediated response;
 KW allergic response; interleukin 18; IL-18; Ige-mediated allergy;
 KW allergic asthma; anaphylactic reaction; asthma associated allergy;
 KW Ige dependent allergic rhinoconjunctivitis.
 XX
 OS Homo sapiens.
 OS

PN WO200168896-A1.
 XX
 PD 20-SEP-2001.
 XX
 PF 02-MAR-2001; 2001MO-US06869.
 XX
 PR 10-MAR-2000; 2000US-0188311.
 XX
 (STRD) UNIV LELAND STANFORD JUNIOR.
 PA
 PI Levy S, Dekruyff RH, Umetsu DT, Maecker H;
 XX
 DR WPI: 2001-570874/64.
 XX
 N-PSDB: AAH78060.
 XX
 PR Reducing antigen specific immune response in conditions such as asthma,
 PT allergic rhinitis, by reducing a T-cell-helper type 2 T cell mediated
 PT antigen-specific allergic response -
 XX
 PS Disclosure: Page 36; 38pp; English.
 XX
 CC The specification describes a method for reducing a T-cell-helper
 CC type 2 (Th2) T cell mediated antigen-specific allergic response. The
 CC method comprises administering a DNA construct encoding a fusion
 CC protein of Interleukin 18 (IL-18) and an antigen associated with the
 CC allergic response. The method is useful for reducing a Th2 T cell
 CC mediated antigen-specific allergic response especially IgE-mediated
 CC allergic asthma or anaphylactic reactions or IgE dependent allergic
 CC rhinoconjunctivitis, and for treating asthma associated allergies where
 CC the allergies are ongoing at the time of the administration. The
 CC present sequence represents a human IL-18, and is used to construct
 CC fusion proteins of the invention.
 XX
 SQ Sequence 193 AA:
 XX
 Query Match 100.0%; Score 816; DB 22; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.6e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLSKLSVIRINLNDVLFIDGGRPLFEDMTDSDCRDNAPRTIFISMYKDSQPRGM 60
 DB 37 YFGKLSKLSVIRINLNDVLFIDGGRPLFEDMTDSDCRDNAPRTIFISMYKDSQPRGM 96
 QY 61 AVTISVCKEISTSCENKIIISFKENPPDNIKDKTSIIFFORSVPGHDNKKMQFESSY 120
 DB 97 AVTISVCKEISTSCENKIIISFKENPPDNIKDKTSIIFFORSVPGHDNKKMQFESSY 156
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYQNEO 157
 DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYQNEO 193
 XX
 RESULT 12
 ID AAM77082
 XX AAM77082 standard; Protein; 193 AA.
 XX
 AC AAM77082;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE Interleukin 18 active protein and precursor.
 XX
 DE Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma; Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity; primary hyperthyroidism.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..36
 FT Peptide /note= "Signal peptide"
 FT 37..193
 FT Peptide

FT /note= "Mature peptide"
 PN EP861663-A2.
 XX
 PD 02-SEP-1998.
 XX
 PF 24-FEB-1998; 98EP-0301352.
 XX
 PR 25-FEB-1997; 97JP-0055468.
 XX
 (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA
 PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
 XX
 DR WPI: 1998-448964/39.
 XX
 N-PSDB: V4828.
 XX
 PR Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity; osteitis,
 PT primary hyperthyroidism and osteoporosis
 XX
 PS Disclosure: Page 24-28; 56pp; English.
 XX
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity; osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SQ Sequence 193 AA:
 XX
 Query Match 99.6%; Score 813; DB 19; Length 193;
 Best Local Similarity 99.4%; Pred. No. 3.5e-83;
 Matches 156; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLSKLSVIRINLNDVLFIDGGRPLFEDMTDSDCRDNAPRTIFISMYKDSQPRGM 60
 DB 37 YFGKLSKLSVIRINLNDVLFIDGGRPLFEDMTDSDCRDNAPRTIFISMYKDSQPRGM 96
 QY 61 AVTISVCKEISTSCENKIIISFKENPPDNIKDKTSIIFFORSVPGHDNKKMQFESSY 120
 DB 97 AVTISVCKEISTSCENKIIISFKENPPDNIKDKTSIIFFORSVPGHDNKKMQFESSY 156
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYQNEO 157
 DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYQNEO 193
 XX
 RESULT 13
 ID AAR99564
 XX AAR99564 standard; Protein; 157 AA.
 XX
 AC AAR99564;
 XX
 DT 29-SEP-1996 (first entry)
 XX
 DE Human interferon-gamma inducer protein.
 XX
 DE Interferon-gamma inducer protein; IFN-gamma; antiviral; virucide;
 KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;
 KW therapy; cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 73
 FT /label= Ile, Thr
 FT 73..193
 FT Peptide EP712931-A2.

```

XX      EP712931-A2.
XX      22-MAY-1996.
XX      10-NOV-1995;      95EP-0308055.
XX      29-SEP-1995;      95JP-0274988.
XX      15-NOV-1994;      94JP-0304203.
XX      23-FEB-1995;      95JP-0058240.
XX      10-MAR-1995;      95JP-0078357.
XX      18-SEP-1995;      95JP-0262062.
XX
XX      (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX      Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
XX      Taniguchi M, Tanimoto T, Torigoe K, Ushio S;
XX      WPI; 1996-252837/26.
XX      N-PSDB; AAT32402.
XX
XX      DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
XX      to treat and prevent, e.g. viral disease, malignancies and immune
XX      disorders
XX
XX      Claim 1; Page 40; 48pp; English.
XX
XX      A novel human protein (AAR9558) induces interferon-gamma (IFN-gamma)
XX      prodn. by immunocompetent cells. It enhances the cytotoxicity of
XX      killer cells and/or induces the formation of killer cells (e.g.
XX      NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic
XX      T-cells). Recombinant IFN-gamma inducer protein can be produced in
XX      high yields using host cells, esp. Escherichia coli, transformed
XX      with a vector carrying the encoding cDNA (AAT32402). It is useful
XX      as an antiviral, antitumor, antibacterial, immunoregulatory and
XX      blood platelet enhancing agent, and can be used in adoptive
XX      immunotherapy. It is also used to raise monoclonal antibodies.
XX      A full-length sequence is given in AAR95560.
XX
XX      Sequence 157 AA:
XX
XX      Query Match          99.4%; Score 811; DB 17; Length 157;
XX      Best Local Similarity 99.4%; Pred. No. 4.5e-83;
XX      Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      1 YFGKESKLSVYRNINDVLFIDQGNRPLEFEDMTDSDCRDNPARTIFITSMYKDSQPRGM 60
XX      1 YFGKESKLSVIRINDVLIFFIDGNNRPIFEIMTSDSDCRDNPRTIFITSMYKDSQPRGM 60
XX      61 AVTIVKCEKISTSTLSCENKIISFKRMNPNDIKTKSDIIFQRSVPGHDNKKMFESSSY 120
XX      61 AVTIVKCEKISTSTLSCENKIISFKRMNPNDIKTKSDIIFQRSVPGHDNKKMFESSSY 120
XX      121 EGYFLACEKERDLEKTLIKKEDELDGRSIMPVONED 157
XX      121 EGYFLACEKERDLEKTLIKKEDELDGRSIMPVONED 157
XX
XX      RESULT 15
XX      AAM15701
XX      ID AAM15701 standard; protein; 157 AA.
XX
XX      AAM15701;
XX
XX      26-JAN-1998 (first entry)
XX
XX      Interferon-gamma inducer protein.
XX
XX      Interferon-gamma, IFN-gamma; antiviral; antitumor; radiotherapy;
XX      immunoregulatory; antitumor agent; chemotherapy; leukopenia;
XX      thrombocytopenia; immunocompetent cell; asthma; hayfever;
XX      rheumatism; interleukin; killer cell.

```


XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 73
FT /label= ile, Thr
XX
XX EP67178-A1.
PN
XX
XX 09-APR-1997.
PD
XX
XX 26-SEP-1996; 96EP-0306997.
PR
XX 20-SEP-1996; 96JP-0269105.
PR 26-SEP-1995; 95JP-0270725.
PR 29-FEB-1996; 96JP-0067434.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX
XX Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
XX
XX WPI; 1997-205381/19.
XX
XX
XX Human protein that induces interferon-gamma prodn. in
PT immuno:competent cells - useful for adoptive immuno:therapy of
PT tumours and as antimicrobial agent etc.
XX
XX
XX Claim 8; Page 20; 26pp; English.
XX
XX The present sequence represents a novel protein from human cells, which
CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.
CC This protein enhances cytotoxicity of Killer cells and induces their
CC formation. It is used as an antitumour agent for antitumour
CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
CC and in the treatment of atopic or immune system diseases, e.g. asthma,
CC hayfever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leukopaenia and thrombocytopaenia associated with
CC radiotherapy or chemotherapy of leukaemia and other cancers. When used in
CC antitumour immunotherapy, this novel protein significantly improves the
CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
CC IL-2 alone, either when administered to the patient (before
CC administration of IL-2) or by addition to the medium in which cells
CC (intended for return to the patient) are being grown.
XX
XX
SQ Sequence 157 AA;

Query Match 99.4%; Score 811; DB 18; Length 157;
Best Local Similarity 98.4%; Pred. No. 4.5e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDVLFIDGNGRPLFEDMTDSDCRDNAPRTITISMYKDSQPRGM 60
DB 1 yfgklesklsvlnndvlfidgngprlffedmtsdcrdnaprtilfismykdsqprgm 60
QY 61 AVTISVKCEKISTLSCENKIISFKENPNPDNIDKTKSDIIFQGRSVPGHDKMKQFESSSY 120
DB 61 avtiskvcekisltscenkliisfkemppndnidktsdliifqgrsvpgdhkmqfesssy 120
QY 121 EGYFLACEKERDLFKILKKEDELDGRSIFMTVONED 157
DB 121 egyflacekerdlfkilkkedeidgrsimftvoned 157

Search completed: June 21, 2002, 09:20:19
Job time: 432 sec

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:46 ; Search time 109.39 Seconds

(without alignments)
137.910 Million cell updates/sec

Title: US-09-780-035-61

Perfect score: 816
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKREDELGDRSIMFTYQNEED 157

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	530	63.7	192	2	S60226
2	85	10.4	381	2	T40341
3	81.5	10.0	270	1	S10532
4	81	9.9	263	2	T39487
5	80.5	9.9	866	2	C71509
6	80.5	9.9	1663	1	C3MS
7	80	9.8	2470	2	T50726
8	79	9.7	452	2	D64583
9	79	9.7	680	2	A28121
10	79	9.7	1772	2	A45352
11	78.5	9.6	204	2	T44357
12	78	9.6	473	2	T33038
13	77.5	9.5	1251	2	A56677
14	77	9.4	364	2	A81261
15	76.5	9.4	425	2	T25457
16	76	9.3	632	2	T00679
17	76	9.3	747	2	E84698
18	75.5	9.3	192	2	S15661
19	75.5	9.3	270	2	I46620
20	75.5	9.3	578	2	A48713
21	75.5	9.3	467	2	H82872
22	75	9.2	467	2	I49609
23	75	9.2	1064	1	S57450
24	74.5	9.1	334	2	T04198
25	74.5	9.1	331	2	E71372
26	74.5	9.1	1036	2	H64245
27	74.5	9.1	1228	2	A57384
28	74.5	9.1	1510	2	T16927
29	74	9.1	245	2	B90488

30	74	9.1	361	2	E96904	mind family ATPase
31	74	9.1	376	2	T24925	hypothetical prote
32	74	9.1	467	2	A47388	serine/threonine p
33	74	9.1	810	2	B71639	virid protein prec
34	74	9.1	2663	1	S28261	centromere protein
35	73.5	9.0	268	2	H85641	probable small sub
36	73.5	9.0	268	2	C90781	probable small sub
37	73.5	9.0	389	2	B69277	TRK potassium upa
38	73.5	9.0	432	2	G90268	conserved hypothet
39	73.5	9.0	475	2	T32036	hypothetical prote
40	73.5	9.0	888	2	A38539	p101 protein precu
41	73.5	9.0	1997	2	F71607	DNA helicase II BR
42	73	8.9	418	2	D82932	seryl-tRNA synthet
43	73	8.9	447	2	T26293	hypothetical prote
44	72.5	8.9	268	1	ICBO1A	interleukin-1 alph
45	72.5	8.9	268	1	B24073	interleukin-1 alph

ALIGNMENTS

RESULT 1
S60226
Cytokine IGIF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S60226
R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torii
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:96061009
A:Accession: S60226
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OKA>
A:Cross-references: EMBL:D49949; NID:q1064822; PIDN:BA08705.1; PID:q1064823
C:Superfamily: Mus musculus cytokine IGIF

Query Match 63.7%; Score 520; DB 2; Length 192;
Best local similarity 65.6%; Pred. No. 1.2e-41;
Matches 101; Conservative 27; Mismatches 24; Indels 2; Gaps 2;
QY 2 PFKLESKLSVIRNLNDQVLFTDQGRPLFEDMTSDCDNAPRTIFITISWKDSOPGMA 61
DB 37 FGRLLCTTAIVIRNLNDQVLEVDK-RQVPEEDMTDQGSASEPQRLITYMKDSEVRELA 95
QY 62 VTISSCKEISTISLSCENKLIIFKEMNPPDNIDKTSDIIFQRSVPGHDKMKOFESSYE 121
DB 96 VTLSSKDSKMSITLSCNNKTIISFEEDMPDENIDDIQSDLIFFQKVPQGH-NKMEFESSLYE 154
QY 122 GYFLACEKERDILFKLLKREDELGDRSIMFTYQNEED 155
DB 155 GHFLACQKEDDAFKLLKREDELGDRSIMFTYQNEED 188
RESULT 2
T40341
hypothetical protein SPBC389.02c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T40341
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z21922
A:Accession: T40341
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-381 <WOO>
A:Cross-references: EMBL:AL022070; PIDN:CA117782.1; GSPDB:GN00067; SPDB:SPBC389.02c
C:Genetics: Experimental source: strain 972h-; cosmid C389

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:48:22 ; Search time 52.75 Seconds

(without alignments)
115.241 Million cell updates/sec

Title: US-09-780-035-61

Perfect score: 816

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....IKKEDLDGRSIMPVQVONED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	816	100.0	193	IL18_HUMAN	Q14116 homo sapien
2	664	81.4	193	IL18_HORSE	Q9XSG7 equus caball
3	659	80.8	193	IL18_BOVIN	Q9TU73 bos taurus
4	642	78.7	192	IL18_PIG	Q19073 sus scrofa
5	618	75.7	193	IL18_CANFA	Q9XST0 canis famili
6	520	63.7	192	IL18_MOUSE	P70380 mus musculu
7	519.5	63.7	194	IL18_RAT	P97636 rattus norv
8	81.5	10.0	270	IL1A_PIG	P18430 sus scrofa
9	81	9.9	267	IL1A_RABIT	P04822 coryctolagus
10	80.5	9.9	1663	CO3_MOUSE	P01027 mus musculu
11	79	9.7	1772	MSPI_PLAYO	P13828 plasmodium
12	77.5	9.5	270	IL1A_HORSE	Q28385 equus caball
13	75.5	9.3	192	OASB_MOUSE	Q60856 mus musculu
14	75	9.2	467	M3K8_MOUSE	Q07174 mus musculu
15	74.5	9.1	351	RPL_TREPA	O83090 treponema p
16	74.5	9.1	1036	Y414_MTCGE	P47653 mycoplasma
17	74.5	9.1	1228	ECM_HUMAN	Q13301 homo sapien
18	74	9.1	270	IL1A_FELCA	Q46613 felis silve
19	74	9.1	467	M3K8_RAT	Q63562 rattus norv
20	74	9.1	2663	CENB_HUMAN	Q02224 homo sapien
21	73	8.9	4590	FATH_HUMAN	Q14517 homo sapien
22	72.5	8.9	268	IL1A_BOVIN	P08831 bos taurus
23	72.5	8.9	313	COL4_ARATH	Q9m8b3 arabidopsis
24	72.5	8.9	467	M3K8_HUMAN	P41279 homo sapien
25	72	8.8	426	YCXC_ASTLO	P58151 astasia lon
26	72	8.8	700	NONA_DROME	Q04947 drosophila
27	72	8.8	800	KINA_YEAST	Q01919 saccharomyc
28	71.5	8.8	268	IL1A_CAPHI	P79161 capra hircu
29	71.5	8.8	375	YC5_CAEEL	Q18610 caenorhabdi
30	71.5	8.8	377	NCK1_HUMAN	P16333 homo sapien
31	71.5	8.8	527	RAG2_HUMAN	P55895 homo sapien
32	71	8.7	198	VS11_ROTNA	P17467 rabbit roca
33	70.5	8.6	268	IL1A_SHEEP	Q28579 ovis aries

ALIGNMENTS

RESULT 1	ID	IL18_HUMAN	STANDARD:	PRT: 193 AA.	09phw6 campylobact
AC	Q14116; 075599;				P53061 saccharomyc
DT	15-JUL-1998 (Rel. 36, Created)				Q61739 mus musculu
DT	15-JUL-1998 (Rel. 36, Last sequence update)				P47037 saccharomyc
DT	01-MAR-2002 (Rel. 41, Last annotation update)				P54787 saccharomyc
DE	Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)				P22523 escherichia
DE	(IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).				P51532 homo sapien
GN	IL18 OR IGIF.				P80093 capsicum an
OS	Homo sapiens (Human).				P53129 saccharomyc
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				P16716 capripoxvir
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				Q9cp43 pasteurella
OX	NCBI_TaxID=9606;				Q9vk89 drosophila
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=96247646; PubMed=8666798;				
RA	Ushio S., Namba M., Okura T., Hattori K., Nakada Y., Akita K.,				
RA	Tanabe F., Kikuchi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,				
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.;				
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression				
RT	in Escherichia coli, and studies on the biologic activities of the				
RT	protein.";				
RT	J. Immunol. 156:4274-4279(1996).				
RL	[2]				
RA	SEQUENCE FROM N.A.				
RT	Yong D., Guixin D., Linhua H., Haitao W.;				
RT	"Cloning and sequencing of the cDNA for precursor hIL-18.";				
RT	Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.				
RL	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Peripheral blood;				
RA	Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;				
RA	Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.				
CC	-I- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS				
CC	AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I				
CC	CELLS.				
CC	-I- SUBCELLULAR LOCATION: Secreted.				
CC	-I- SIMILARITY: BELONGS TO THE IL-18 FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	EMBL; D49950; BAA08706.1; -				
CC	EMBL; AF077611; AAC27787.1; -				
DR					

DR EMBL: AY044641; AAK95950.1; -
DR EMBL: U90434; AAB50010.1; -
DR MIM: 600953; -
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
KW cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CONFLICT 66 66 F->L (IN REF. 2).
FT CONFLICT 86 86 S->R (IN REF. 2).
FT CONFLICT 191 191 N->S (IN REF. 2).
SQ SEQUENCE 193 AA; 22326 MW; 323062C20378BD55 CRC64;

Query Match 100.0%; Score 816; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.6e-68;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTDSDCRDNAPRTIFITSMYKDSQPRGM 60
ID IL18_HORSE STANDARD; PRT; 193 AA.
AC Q9XSQ7;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN NM [1]
RP SEQUENCE FROM N.A.
RA Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs";
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC
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CC
DR EMBL: Y11131; CAA72013.1; -
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E904ECAP CRC64;

Query Match 81.4%; Score 664; DB 1; Length 193;

Best Local Similarity 78.3%; Pred. No. 1.7e-54;
Matches 123; Conservative 21; Mismatches 13; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTDSDCRDNAPRTIFITSMYKDSQPRGM 60
ID IL18_BOVIN STANDARD; PRT; 193 AA.
AC Q9N7J3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN NM [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20012648; PubMed-10547157;
RA Shoda L.R., Zarlega D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC
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CC
DR EMBL: AF124789; AAF08686.1; -
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.8%; Score 659; DB 1; Length 193;
Best Local Similarity 77.7%; Pred. No. 4.9e-54;
Matches 122; Conservative 23; Mismatches 12; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFEDMTDSDCRDNAPRTIFITSMYKDSQPRGM 60
ID IL18_BOVIN STANDARD; PRT; 193 AA.
AC Q9N7J3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN NM [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20012648; PubMed-10547157;
RA Shoda L.R., Zarlega D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC
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CC
DR EMBL: AF124789; AAF08686.1; -
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:27 ; Search time 194.32 Seconds
(without alignments)
139.771 Million cell updates/sec

Title: US-09-780-035-61
Sequence: 1 YFGKLESKLSVIRNLNDQVL.....LKKREDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	803	98.4	193	4 Q96KJ8	Q96KJ8 homo sapien
2	797	97.7	193	6 Q9BG15	Q9BG15 macaca mula
3	659	80.8	178	6 Q9MZ18	Q9MZ18 bos taurus
4	653	80.0	193	6 Q9G109	Q9G109 ovis aries
5	639	78.3	192	6 Q9SM33	Q9SM33 felis silve
6	631	77.3	192	6 Q9N1P7	Q9N1P7 sus scrofa
7	446	54.7	196	11 Q91266	Q91266 simodon hi
8	318	39.0	84	6 Q951E7	Q951E7 canis famli
9	204	25.0	45	4 Q9ND49	Q9ND49 homo sapien
10	192	23.5	211	13 Q98SQ1	Q98SQ1 anas platyr
11	181.5	22.2	198	13 Q91BD2	Q91BD2 gallus gall
12	88	10.8	4643	5 Q9VW71	Q9VW71 drosophila
13	85	10.4	381	3 Q43031	Q43031 schizosacch
14	81.5	10.0	617	5 Q25986	Q25986 plasmodium
15	81.5	10.0	1049	2 Q93KF0	Q93KF0 caldicellul
16	81	9.9	263	3 Q74316	Q74316 schizosacch

17	80.5	9.9	866	16 Q84500	Q84500 chlamydia t
18	80	9.8	2470	13 Q90681	Q90681 gallus gall
19	79.5	9.7	1044	3 Q94173	Q94173 pneumocysti
20	79	9.7	452	16 Q25249	Q25249 helicobacte
21	78.5	9.6	204	2 Q92N77	Q92N77 clostridium
22	78.5	9.6	595	10 Q9SDM4	Q9SDM4 dunaliella
23	78	9.6	473	5 Q16673	Q16673 caenorhabdi
24	77.5	9.5	454	6 Q9BGD1	Q9BGD1 mtrconylet
25	77.5	9.5	840	12 Q9QBA2	Q9QBA2 yaba monkey
26	77.5	9.5	1251	13 Q91365	Q91365 coturnix co
27	77	9.4	364	16 Q9PM33	Q9PM33 campylobact
28	77	9.4	847	4 Q9N1C1	Q9N1C1 homo sapien
29	76.5	9.4	425	5 P90990	P90990 caenorhabdi
30	76.5	9.4	454	6 Q9BG48	Q9BG48 sturnira il
31	76	9.3	632	10 Q80569	Q80569 arabidopsis
32	76	9.3	747	10 Q82393	Q82393 arabidopsis
33	75.5	9.3	454	6 Q9BGE4	Q9BGE4 erophylla s
34	75.5	9.3	454	6 Q9BGB7	Q9BGB7 phyllostomu
35	75.5	9.3	578	16 Q9PPR7	Q9PPR7 uraplasma
36	75	9.2	445	13 Q57610	Q57610 scyllorhinu
37	75	9.2	1064	13 Q90601	Q90601 gallus gall
38	75	9.2	1247	5 Q95QV2	Q95QV2 caenorhabdi
39	74.5	9.1	137	5 Q77077	Q77077 plasmodium
40	74.5	9.1	334	10 Q9ZSB9	Q9ZSB9 arabidopsis
41	74.5	9.1	454	6 Q9BGB8	Q9BGB8 phylloncyte
42	74.5	9.1	454	6 Q9BGB1	Q9BGB1 saccolteryx
43	74.5	9.1	974	11 Q924W2	Q924W2 rattus norv
44	74.5	9.1	1510	5 Q22699	Q22699 caenorhabdi
45	74	9.1	245	17 Q97UG0	Q97UG0 sulfolobus

ALIGNMENTS

RESULT 1
Q96KJ8 PRELIMINARY: PRT: 193 AA.
ID Q96KJ8
AC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA."
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF380360; AAK57024.1;
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match	Score	DB 4:	Length
Best Local Similarity	98.4%	803	193
Matches 154; Conservative	2;	Mismatches 1;	Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFDGGRPLFEDMTSDCRDNAPRTIFISYKDSOPRGM 60			
DB 37 YFGKLESKLSVIRNLNDQVLFDGGRPLFEDMTSDCRDNAPRTIFISYKDSOPRGM 96			
QY 61 AVTISVCKEISTLSCENKIISFKEMNPDPNIDKTSIDIFFORSVPGHDKMKOFESSSY 120			
DB 97 AVTISVCKEISTLSCENKIISFKEMNPDPNIDKTSIDIFFORSVPGHDKMKOFESSSY 156			
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157			
DB 157 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 193			
RESULT 2			

Q9BG15 PRELIMINARY; PRT; 193 AA.
 ID Q9BG15
 AC Q9BG15
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE INTERLEUKIN-18.
 GN IL18.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCBITaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21229850; PubMed=11331040;
 RA Glavedoni L.D., Imhof J.D., Parodi L.M., Velasquillo C.M.,
 RA Hodara V.L.;
 RT "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
 RT Simian Immunodeficiency Virus Does Not Result in Increased Viral
 RT Replication";
 RL J. Interferon Cytokine Res. 21:173-180(2001).
 DR EMBL: AF303732; AAK13416.1;
 SQ SEQUENCE 193 AA; 22325 MW; B2BD29C033B80B5E CRC64;

Query Match 97.7%; Score 797; DB 6; Length 193;
 Best Local Similarity 96.2%; Pred. No. 1.2e-72;
 Matches 151; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRLNQVLFIDGNNRPLFEDMTSDCCRNAPRTITITSMYKDSQPRGM 60
 DB 37 YFGKLESKLSVIRLNQVLFIDGNNRPLFEDMTSDCCRNAPRTITITSMYKDSQPRGM 96
 QY 61 AVTISVCKEISTLSCENKTIISFKENPPDNINKDTSIIFFQSVPGHDKMQFESSY 120
 DB 97 AVTISVCKEISTLSCENKTIISFKENPPDNINKDTSIIFFQSVPGHDKMQFESSY 156
 QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
 DB 157 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 193

RESULT 3
 Q9MZL8 PRELIMINARY; PRT; 178 AA.
 ID Q9MZL8
 AC Q9MZL8
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE INTERLEUKIN-18 (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCBITaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY, LIVER, BLOOD MONONUCLEAR CELLS;
 RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrl M., Bolin C.A.;
 RT "Cloning of bovine interleukin-18, expression in Escherichia coli, and
 RT characterization of the biologic activities of the recombinant
 RT cytokine";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF173175; AAF89833.1;
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1.
 FT NON_TER 178
 FT 178
 SQ SEQUENCE 178 AA; 20631 MW; 816D6B2888ACB497 CRC64;

Query Match 80.8%; Score 659; DB 6; Length 178;

Best Local Similarity 77.7%; Pred. No. 8.9e-59;
 Matches 122; Conservative 23; Mismatches 12; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRLNQVLFIDGNNRPLFEDMTSDCCRNAPRTITITSMYKDSQPRGM 60
 DB 22 HFGKLEPKLSIIRLNQVLFIDGNNRPLFEDMTSDCCRNAPRTITITSMYKDSQPRGM 81
 QY 61 AVTISVCKEISTLSCENKTIISFKENPPDNINKDTSIIFFQSVPGHDKMQFESSY 120
 DB 82 AVTISVCKEISTLSCENKTIISFKENPPDNINKDTSIIFFQSVPGHDKMQFESSY 141
 QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
 DB 142 KGYFLACKKENDLFKLLKKEDELGDRSIMFTVQNE 178

RESULT 4
 Q9GL09 PRELIMINARY; PRT; 193 AA.
 ID Q9GL09
 AC Q9GL09
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE INTERLEUKIN-18 (IGIF).
 GN IL-18.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NC NCBITaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
 RT "Cloning of ovine interleukin 18 cDNA";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ401033; CAC09326.2;
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1.
 SQ SEQUENCE 193 AA; 22166 MW; CCDOA329062EF18C CRC64;

Query Match 80.0%; Score 653; DB 6; Length 193;
 Best Local Similarity 78.3%; Pred. No. 3.9e-58;
 Matches 123; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRLNQVLFIDGNNRPLFEDMTSDCCRNAPRTITITSMYKDSQPRGM 60
 DB 37 HFGKLEPKLSIIRLNQVLFIDGNNRPLFEDMTSDCCRNAPRTITITSMYKDSQPRGM 96
 QY 61 AVTISVCKEISTLSCENKTIISFKENPPDNINKDTSIIFFQSVPGHDKMQFESSY 120
 DB 97 AVTISVCKEISTLSCENKTIISFKENPPDNINKDTSIIFFQSVPGHDKMQFESSY 156
 QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157
 DB 157 KGYFLACKKENDLFKLLKKEDELGDRSIMFTVQNE 193

RESULT 5
 Q95M33 PRELIMINARY; PRT; 192 AA.
 ID Q95M33
 AC Q95M33
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE INTERFERON-GAMMA INDUCING FACTOR.
 GN IGIF.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NC NCBITaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:49 ; Search time 84.18 Seconds
(without alignments)
45.555 Million cell updates/sec

Title: US-09-780-035-61

Sequence: 1 YFGKLESLKSLVIRNLNDQVL.....LKKEDELGRSIFMTYQNEED 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCRTS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81.1	99.4	157	2	US-08-896-605A-6
2	81.1	99.4	157	2	US-08-896-605A-6
3	81.1	99.4	157	3	US-08-884-324-1
4	81.1	99.4	157	3	US-08-996-338-26
5	81.1	99.4	157	4	US-08-558-818-1
6	81.1	99.4	157	4	US-08-974-469A-1
7	81.1	99.4	157	4	US-08-832-180-1
8	81.1	99.4	157	4	US-08-832-198-6
9	81.1	99.4	193	2	US-08-896-605A-2
10	81.1	99.4	193	2	US-08-896-501A-2
11	81.1	99.4	193	4	US-08-832-180-9
12	81.1	99.4	157	2	US-08-502-535B-2
13	81.1	99.4	157	2	US-08-908-005A-2
14	81.1	99.4	157	3	US-08-996-338-27
15	81.1	99.4	157	4	US-08-558-818-7
16	81.1	99.4	157	4	US-08-974-469A-7
17	81.1	99.4	157	4	US-08-832-180-8
18	81.1	99.4	157	4	US-08-832-198-11
19	81.1	99.4	157	4	US-09-253-523-2
20	81.1	99.4	157	4	US-09-251-911-2
21	81.1	99.4	50	4	US-08-832-198-2
22	81.1	99.4	25	4	US-08-558-818-4
23	81.1	99.4	25	4	US-08-974-469A-4
24	81.1	99.4	25	4	US-08-832-180-4
25	81.1	99.4	25	4	US-08-832-198-8
26	81.1	99.4	17	4	US-08-832-198-5
27	81.1	99.4	155	6	5494663-8

28	81.1	9.9	267	6	5494663-5	Patent No. 5494663
29	77.5	9.5	270	2	US-08-611-880-1	Sequence 1, Appl
30	77.5	9.5	270	4	US-09-085-305-13	Sequence 13, Appl
31	75.5	9.3	270	4	US-09-085-305-20	Sequence 20, Appl
32	74.5	9.1	270	4	US-09-085-305-14	Sequence 14, Appl
33	73.5	9.0	855	2	US-08-482-090-12	Sequence 12, Appl
34	73.5	9.0	856	2	US-08-481-700B-8	Sequence 8, Appl
35	73.5	9.0	856	2	US-09-007-383-16	Sequence 16, Appl
36	72.5	8.9	268	4	US-09-085-305-8	Sequence 8, Appl
37	72.5	8.9	268	4	US-09-085-305-18	Sequence 18, Appl
38	72.5	8.9	1294	2	US-08-819-288-3	Sequence 3, Appl
39	72.5	8.9	1294	4	US-08-400-348-3	Sequence 3, Appl
40	72.5	8.9	1321	1	US-08-261-822A-3	Sequence 3, Appl
41	72.5	8.9	1321	5	PCT-US95-07744A-3	Sequence 3, Appl
42	71.5	8.8	268	4	US-09-085-305-10	Sequence 10, Appl
43	71.5	8.8	3418	4	US-08-755-587-44	Sequence 44, Appl
44	71.5	8.7	14	4	US-08-832-198-4	Sequence 4, Appl
45	71.5	8.7	1588	5	PCT-US93-07261-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-896-605A-6
Sequence 6, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 July 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-605A-6
Query Match 99.4%; Score 81.1; DB 2; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0;

QY 1 YFGKLESKLSVIRNLNDQVLEFDQGNRPLEFEDMTSDSCRDNAFRTIIFIISMVKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNLNDQVLEFDQGNRPLEFEDMTSDSCRDNAFRTIIFIISMVKDSQPRGM 60
 QY 61 AVTISVCKEISTLSCENKTIISFKENPPDNKDKTSDIIFQRSVPGHDKMKQFESSSY 120
 DB 61 AVTISVCKEISTLSCENKTIISFKENPPDNKDKTSDIIFQRSVPGHDKMKQFESSSY 120
 QY 121 EGYFLACEKERDLFKLLIKKEDLGDRSIMFTYONED 157
 DB 121 EGYFLACEKERDLFKLLIKKEDLGDRSIMFTYONED 157

RESULT 2

US-08-896-501A-4
 ; Sequence 4, Application US/08896501A
 ; Patent No. 5891663
 ; GENERAL INFORMATION:
 ; APPLICANT: TANIMOTO, Tadao
 ; APPLICANT: KURIMOTO, Masashi
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/896,501A
 ; FILING DATE: 18-JUL-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 213,267/1996
 ; FILING DATE: 25-JUL-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 31,474/1997
 ; FILING DATE: 31-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: TANIMOTO-3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 157 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-896-501A-4

Query Match 99.4%; Score 811; DB 2; Length 157;
 Best Local Similarity 99.4%; Pred. No. 5,4e-88;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLEFDQGNRPLEFEDMTSDSCRDNAFRTIIFIISMVKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNLNDQVLEFDQGNRPLEFEDMTSDSCRDNAFRTIIFIISMVKDSQPRGM 60
 QY 61 AVTISVCKEISTLSCENKTIISFKENPPDNKDKTSDIIFQRSVPGHDKMKQFESSSY 120
 DB 61 AVTISVCKEISTLSCENKTIISFKENPPDNKDKTSDIIFQRSVPGHDKMKQFESSSY 120

QY 121 EGYFLACEKERDLFKLLIKKEDLGDRSIMFTYONED 157
 DB 121 EGYFLACEKERDLFKLLIKKEDLGDRSIMFTYONED 157

RESULT 3

US-08-884-324-1
 ; Sequence 1, Application US/08884324
 ; Patent No. 6060283
 ; GENERAL INFORMATION:
 ; APPLICANT: Takanori OKURA
 ; APPLICANT: Kakuji TORIGOE
 ; APPLICANT: Masashi KURIMOTO
 ; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
 ; TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/884,324
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 185,305/96
 ; FILING DATE: 27-JUN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: OKURA-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 157 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-884-324-1

Query Match 99.4%; Score 811; DB 3; Length 157;
 Best Local Similarity 99.4%; Pred. No. 5,4e-88;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLEFDQGNRPLEFEDMTSDSCRDNAFRTIIFIISMVKDSQPRGM 60
 DB 1 YFGKLESKLSVIRNLNDQVLEFDQGNRPLEFEDMTSDSCRDNAFRTIIFIISMVKDSQPRGM 60
 QY 61 AVTISVCKEISTLSCENKTIISFKENPPDNKDKTSDIIFQRSVPGHDKMKQFESSSY 120
 DB 61 AVTISVCKEISTLSCENKTIISFKENPPDNKDKTSDIIFQRSVPGHDKMKQFESSSY 120
 QY 121 EGYFLACEKERDLFKLLIKKEDLGDRSIMFTYONED 157
 DB 121 EGYFLACEKERDLFKLLIKKEDLGDRSIMFTYONED 157

RESULT 4

US-08-996-338-26
 ; Sequence 26, Application US/08996338
 ; Patent No. 6087116
 ; GENERAL INFORMATION:

APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takamori
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-JUL-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-3528
TELEFAX: 202-737-3528
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-26

Query Match 99.4%; Score 811; DB 3; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDRNAFRTFIISWKDSOPRGM 60
DB 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDRNAFRTFIISWKDSOPRGM 60
QY 61 AVTISVCKEISTLSCENKTIISFKEMNPDPNIDKTSKDIIFFORSVPGHDKMKQFESSSY 120
DB 61 AVTISVCKEISTLSCENKTIISFKEMNPDPNIDKTSKDIIFFORSVPGHDKMKQFESSSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 5
US-08-558-818-1
Sequence 1, Application US/08558818
Patent No. 6197297
GENERAL INFORMATION:
APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUO
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo

APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,818
FILING DATE:
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION DATA: JP 58,240/95
PRIORITY APPLICATION DATA: February 23, 1995
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-558-818-1

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDRNAFRTFIISWKDSOPRGM 60
DB 1 YFGKLESKLSVIRNNDQVLFIDQGNRPFLFEDMTSDCDRNAFRTFIISWKDSOPRGM 60
QY 61 AVTISVCKEISTLSCENKTIISFKEMNPDPNIDKTSKDIIFFORSVPGHDKMKQFESSSY 120
DB 61 AVTISVCKEISTLSCENKTIISFKEMNPDPNIDKTSKDIIFFORSVPGHDKMKQFESSSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 6
US-08-974-469A-1
Sequence 1, Application US/08974469A
Patent No. 6207641
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUO
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: FUKUDA, Shigeharu
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,469A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,879
FILING DATE:
APPLICATION NUMBER: JP 78,357/95
FILING DATE: March 10, 1995
APPLICATION NUMBER: JP 274,988/95
FILING DATE: September 29, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-469A-1

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDVLFIDQGNRPLEFEDMTSDCRDNPRTIFIIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDVLFIDQGNRPLEFEDMTSDCRDNPRTIFIIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISTLSCENKIIISFKENPPDNIKDKTSDIIFQSVGHDNKKQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIIISFKENPPDNIKDKTSDIIFQSVGHDNKKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 157

RESULT 7
US-08-832-180-1
Sequence 1, Application US/08832180
Patent No. 6214584
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: USHIO, Shimpai
APPLICANT: TORIGOE, Kakui
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584member 15, 1994
APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-1

Query Match 99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDVLFIDQGNRPLEFEDMTSDCRDNPRTIFIIISMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDVLFIDQGNRPLEFEDMTSDCRDNPRTIFIIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISTLSCENKIIISFKENPPDNIKDKTSDIIFQSVGHDNKKQFESSY 120
DB 61 AVTISVKCEKISTLSCENKIIISFKENPPDNIKDKTSDIIFQSVGHDNKKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 157

RESULT 8
US-08-832-198-6
Sequence 6, Application US/08832198
Patent No. 6242255
GENERAL INFORMATION:
APPLICANT: AKIRA, Kenji
APPLICANT: NUKADA, Yoshiyuki
APPLICANT: FUJII, Mitsukiyo
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
TITLE OF INVENTION: PRODUCTION BY IMMUNOCOMPETENT CELL
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,198
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
; FILING DATE: 29-FEB-1996
; APPLICATION NUMBER: JP not yet received
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: AKITA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" in position 73 is either
; OTHER INFORMATION: 'Ile' or 'Thr'
;
; US-08-832-198-6

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Query Match          99.4%; Score 811; DB 4; Length 157;
Best Local Similarity 99.4%; Pred. No. 5.4e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDGNNRPLFEDMTSDCDNAPRTIIFITISMYKDSOPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDGNNRPLFEDMTSDCDNAPRTIIFITISMYKDSOPRGM 60
QY 61 AVTISVCEKISTLSCENKTIISFEKEMNPPDNIKDKTSDIIFQKRSVPGHDNKMGESESSY 120
DB 61 AVTISVCEKISTLSCENKTIISFEKEMNPPDNIKDKTSDIIFQKRSVPGHDNKMGESESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 157

RESULT 9
US-08-896-605A-2
; Sequence 2, Application US/08896605A
; Patent No. 5879942
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,605A
; FILING DATE: 18 JULY 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207,691/1996
; FILING DATE: 19-JUL-1996
; APPLICATION NUMBER: JP 156,062/1997
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-896-605A-2

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Query Match          99.4%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDGNNRPLFEDMTSDCDNAPRTIIFITISMYKDSOPRGM 60
DB 37 YFGKLESKLSVIRNLNDQVLFIDGNNRPLFEDMTSDCDNAPRTIIFITISMYKDSOPRGM 96
QY 61 AVTISVCEKISTLSCENKTIISFEKEMNPPDNIKDKTSDIIFQKRSVPGHDNKMGESESSY 120
DB 97 AVTISVCEKISTLSCENKTIISFEKEMNPPDNIKDKTSDIIFQKRSVPGHDNKMGESESSY 156
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 157
DB 157 EGYFLACEKERDLFKLILKKEDELGDRSIMFTYONED 193

RESULT 10
US-08-896-501A-2
; Sequence 2, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 31,474/1997
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-501A-2

Query Match 99.4%; Score 811; DB 2; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSYIRNLNDQVLFIDGKRPLEDMTSDCDRNAPRTIFITISMYKDSQPRGM 60
DB 37 YFGKLESKLSYIRNLNDQVLFIDGKRPLEDMTSDCDRNAPRTIFITISMYKDSQPRGM 96
QY 61 AVTISVCKEKISTLSCENKTIISFKENPNPDNIKDKTSDIIFORSVPGHDKMKQFESSY 120
DB 97 AVTISVCKEKISTLSCENKTIISFKENPNPDNIKDKTSDIIFORSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLPFLIKKEDDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLPFLIKKEDDELGDRSIMFTVQNE 193

RESULT 11
US-08-832-180-9
Sequence 9, Application US/08832180
Patent No. 6214584

GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAKAKU
APPLICANT: KENKYUO
APPLICANT: USHIO, Shimpel
APPLICANT: TORIGOE, Kakuji
APPLICANT: TANIMOTO, Tadao
APPLICANT: OKAMURA, Haruki
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,180
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/558,191
FILING DATE:
APPLICATION NUMBER: JP 304,203/94
FILING DATE: No. 6214584member 15, 1994

APPLICATION NUMBER: 10048102
FILING DATE: September 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: USHIO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-832-180-9

Query Match 99.4%; Score 811; DB 4; Length 193;
Best Local Similarity 99.4%; Pred. No. 7.2e-88;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSYIRNLNDQVLFIDGKRPLEDMTSDCDRNAPRTIFITISMYKDSQPRGM 60
DB 37 YFGKLESKLSYIRNLNDQVLFIDGKRPLEDMTSDCDRNAPRTIFITISMYKDSQPRGM 96
QY 61 AVTISVCKEKISTLSCENKTIISFKENPNPDNIKDKTSDIIFORSVPGHDKMKQFESSY 120
DB 97 AVTISVCKEKISTLSCENKTIISFKENPNPDNIKDKTSDIIFORSVPGHDKMKQFESSY 156
QY 121 EGYFLACEKERDLPFLIKKEDDELGDRSIMFTVQNE 157
DB 157 EGYFLACEKERDLPFLIKKEDDELGDRSIMFTVQNE 193

RESULT 12
US-08-502-535B-2
Sequence 2, Application US/08502535B
Patent No. 5912324

GENERAL INFORMATION:
APPLICANT: OKAMURA, Haruki
APPLICANT: TANIMOTO, Tadao
APPLICANT: TORIGOE, Kakuji
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/502,535B
FILING DATE: 14-JUL-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184162/1994
FILING DATE: 14-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 45057/1995
FILING DATE: 10-FEB-1995

GENERAL INFORMATION:
 APPLICANT: TORIGOE, Kakuji
 APPLICANT: OKURA, Takao-ri
 APPLICANT: KURIMOTO, Masashi
 TITLE OF INVENTION: POLYPEPTIDES
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEWMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 City: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/996,338
 FILING DATE: 22-DEC-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 74,697/1997
 FILING DATE: 12-MAR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 215,488/1997
 FILING DATE: 28-JUL-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 291,837/1997
 FILING DATE: 09-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25,618
 REFERENCE/DOCKET NUMBER: TORIGOE-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 157
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-27

Query Match 63.5%; Score 518; DB 3; Length 157;
Best Local Similarity 65.6%; Pred. No. 1.8e-53;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGLKLSKLSVIRNINDQVLFIDGNRPLFEDMTDSDCRDNPRTIIFLISMYKDSOPRGMA 61
||:| :|||:|||||:| :|:||||| :|:| |||:||||: ||:|
Db 2 FGLHCTTAVIRININDQVLFVDK-RQPVFEDMTDIDQASSEPQTRLIIYMYKDSVARGIA 60
QY 62 VTISVCKEISTLSCENKIISFEKMPDPNIDKTSDIIFQORSVPGHDKMKQFESSSYE 121
||:| | |||:|||||:|:|:| :||:||||| :||:||||| :||:||||| :||:|||||
Db 61 VTLSVKDSKXSTLSCKNKIISFEEMDPENIDIDQSLIFFQKRVPGH-NKMEFESSLYE 119
QY 122 GYFLACEKERDLFKLLKKEDELGDRSIMFTYQN 155
|:||||| :| |||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
Db 120 GHFLACQKEDDAFKLLKKNKDENGDKSVMTLTN 153

RESULT 15

US-08-558-818-7
Sequence 7, Application US/08558818
Patent No. 6197297

GENERAL INFORMATION:

APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
APPLICANT: KENKYUJO
APPLICANT: KUNIKATA, Toshio
APPLICANT: TANIGUCHI, Mutsuko
APPLICANT: KOHNO, Keizo
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
WHICH INDUCES INTERFERON- PRODUCTION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect Version 5.0
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FELICIT-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558, 818

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA: JP 58,240/95

PRIOR APPLICATION DATA: February 23, 1995

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: mouse
INDIVIDUAL ISOLATE: liver
US-08-558-818-7

Query Match 63.5%; Score 518; DB 4; Length 157;
Best Local Similarity 65.6%; Pred. No. 1.8e-53;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGLKLSKLSVIRNINDQVLFIDGNRPLFEDMTDSDCRDNPRTIIFLISMYKDSOPRGMA 61
||:| :|||:|||||:| :|:||||| :|:| |||:||||: ||:|
Db 2 FGLHCTTAVIRININDQVLFVDK-RQPVFEDMTDIDQASSEPQTRLIIYMYKDSVARGIA 60
QY 62 VTISVCKEISTLSCENKIISFEKMPDPNIDKTSDIIFQORSVPGHDKMKQFESSSYE 121
||:| | |||:|||||:|:|:| :||:||||| :||:||||| :||:||||| :||:|||||
Db 61 VTLSVKDSKXSTLSCKNKIISFEEMDPENIDIDQSLIFFQKRVPGH-NKMEFESSLYE 119
QY 122 GYFLACEKERDLFKLLKKEDELGDRSIMFTYQN 155
|:||||| :| |||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
Db 120 GHFLACQKEDDAFKLLKKNKDENGDKSVMTLTN 153

Search completed: June 21, 2002, 09:21:50
Job time: 413 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:33 ; Search time 14.09 Seconds

(without alignments)
81.836 Million cell updates/sec

Title: US-09-780-035-3

Perfect score: 68

Sequence: 1 PLEFDMTSDCR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1579

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	30.9	8	2 A32523	peptidyl-di-peptida
2	19	27.9	11	2 A29806	acidic proline-rich
3	18	26.5	11	2 D42965	tailin - chicken (f
4	18	26.5	11	2 PT0229	Ig heavy chain CDR
5	18	26.5	12	2 PC4377	telomeric and tetr
6	17	25.0	6	2 I67345	MHC H2-K-K cell su
7	17	25.0	10	2 PX0060	lysosome-associate
8	17	25.0	11	1 GMR0L	leucosulfakinin -
9	17	25.0	11	1 B49164	chromogranin-B - r
10	17	25.0	11	2 A57458	gene Gax protein -
11	17	25.0	11	2 S58244	pyrrolidinovaline q
12	17	25.0	11	2 I33098	173k exoantigen -
13	17	25.0	12	2 JQ2318	hypothetical 1.4K
14	17	25.0	12	2 A09985	gamma-crystallin -
15	16	23.5	6	2 PT0652	T-cell receptor be
16	16	23.5	2	2 S68004	hucolin, 75k chain
17	16	23.5	9	2 JN0026	sperm-activating p
18	16	23.5	9	2 S36898	ribosomal protein
19	16	23.5	9	2 JN0027	[Phe-6]-mosact - s
20	16	23.5	10	2 GXH01	gastric juice pept
21	16	23.5	10	2 JN0025	mosact - sea urchi
22	16	23.5	10	2 A61354	carliline medium/1
23	16	23.5	11	2 B29806	acidic proline-rich
24	16	23.5	12	1 UOGM2	urotensin II - ion
25	16	23.5	12	1 S42765	urotensin II - tel
26	16	23.5	12	2 JS0423	urotensin II-A pep
27	16	23.5	12	2 A61309	glycoprotein hormo
28	16	23.5	12	2 A54315	entactin/nidogen -
29	16	23.5	12	2 A54315	

30	16	23.5	12	2 S74144	aggreacan - bovine
31	16	23.5	12	2 D85517	unknown protein en
32	15	22.1	6	2 A27696	contraction-inhibi
33	15	22.1	6	2 B27696	contraction-inhibi
34	15	22.1	8	2 PN0043	phosphatidylethano
35	15	22.1	9	2 S66419	tetrameric protein
36	15	22.1	10	1 SPPGK	neuromedin K - pig
37	15	22.1	10	2 JN0024	neurokinin A - chl
38	15	22.1	10	2 S62208	polyferredoxin - M
39	15	22.1	10	2 A56633	neomysuppressin -
40	15	22.1	11	2 S04875	nifs protein - Bra
41	15	22.1	11	2 S71304	amine oxidase (cop
42	15	22.1	12	2 S07206	kassinin - Senegal
43	15	22.1	12	2 C39109	hypothetical 1.2K
44	15	22.1	12	2 A61503	sterol carrier pro
45	15	22.1	12	2 PH1605	Ig H chain V-D-J r

ALIGNMENTS

RESULT 1
A32523
peptidyl-di-peptidase A (PC 3.4.15.1) - bovine (fragment)
N.Alternate names: angiotensin I-converting enzyme; peptidyl-di-peptidase I
C.Species: Bos primigenius taurus (cattle)
C.Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 11-May-2000
C.Accession: A32523
R.Harris, R.B.
Adv. Exp. Med. Biol. 198, 513-521, 1986
A.Title: Isolation and sequencing of an active-site peptide from angiotensin I-conver
A.Reference number: A32523; MUID:87123961
A.Accession: A32523
A.Molecule type: protein
A.Residues: 1-8 <HAR>
C.Superfamily: mammalian peptidyl-di-peptidase A
C.Keywords: alternative splicing; blood pressure control; peptidyl-di-peptide hydrolase

Query Match 30.9%; Score 21; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEEDMTSD 10

DB 1 FEELADSE 8

RESULT 2

A29806
acidic proline-rich protein HP43b - golden hamster (fragment)

C.Species: Mesocricetus auratus (golden hamster)

C.Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993

C.Accession: A29806

R.Mehansho, H.; Ann, D.K.; Butler, L.G.; Rogler, J.; Carlson, D.M.

J. Biol. Chem. 262, 12344-12350, 1987

A.Title: Induction of proline-rich proteins in hamster salivary glands by isoproteren

A.Reference number: A92611; MUID:87308247

A.Accession: A29806

A.Molecule type: protein

A.Residues: 1-11 <MEH>

Query Match 27.9%; Score 19; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LFEDMTDS 9

DB 3 LYEDSPXS 10

RESULT 3

D42965
 talin - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
 C:Accession: D42965
 R:Hagmann, J.; Grob, M.; Burger, M.M.
 J. Biol. Chem. 267, 14424-14428, 1992
 A:Title: The cytoskeletal protein talin is O-glycosylated.
 A:Reference number: A42965; MUID:92332560
 A:Accession: D42965
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <HAG>

Query Match 26.5%; Score 18; DB 2; Length 11;
 Best Local Similarity 37.5%; Pred. No. 4.1e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LFEDMTDS 9
 :| |:
 Db 2 IFSSMGDA 9

RESULT 4
 PT0229
 Ig heavy chain CDR3 region (clone 1-115) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0229
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337
 A:Accession: PT0229
 A:Molecule type: DNA
 A:Residues: 1-11 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 26.5%; Score 18; DB 2; Length 11;
 Best Local Similarity 22.2%; Pred. No. 4.1e+03;
 Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLFEDMTDS 9
 |::|:
 Db 3 PYDYDILTEN 11

RESULT 5
 PC4377
 telomeric and tetraplex DNA binding protein qTP42 VIII - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
 C:Accession: PC4377
 R:Sari, G.; Weisman-Shomer, P.; Fry, M.
 Biochem. Biophys. Res. Commun. 237, 611-623, 1997
 A:Title: Telomeric and tetraplex DNA binding properties of qTP42: A homologue of the CA
 A:Reference number: PC4371; MUID:97445086
 A:Accession: PC4377
 A:Molecule type: protein
 A:Residues: 1-12 <SAR>
 C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 26.5%; Score 18; DB 2; Length 12;
 Best Local Similarity 33.3%; Pred. No. 4.5e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 FEDMTSDC 11
 |::|:
 Db 4 FHVSGSKC 12

RESULT 6
 I67345
 MHC H2-K-k cell surface glycoprotein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: I67345
 R:Archibald, A.L.; Thompson, N.A.; Kvist, S.
 EMBO J. 5, 957-965, 1986
 A:Title: A single nucleotide difference at the 3' end of an intron causes differential
 A:Reference number: I53243; MUID:86247587
 A:Accession: I67345
 A:Molecule type: DNA
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-6 <RES>
 A:Cross-references: GB:M26859; NID:9199439; PIDN:AAA39612.1; PID:g387458
 A:Genetics:
 A:Introns: 6/1
 C:Keywords: glycoprotein

Query Match 25.0%; Score 17; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 DCR 12
 ||:
 Db 3 DCK 5

RESULT 7
 PX0060
 lysosome-associated membrane glycoprotein 2 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-1995
 C:Accession: PX0060
 R:Akasaki, K.; Yamaguchi, Y.; Furuno, K.; Tsuji, H.
 J. Biochem. 110, 922-927, 1991
 A:Title: Purification, some properties, and tissue distribution of a major lysosome-a
 A:Reference number: PX0060; MUID:92176167
 A:Accession: PX0060
 A:Molecule type: protein
 A:Residues: 1-10 <AKA>
 A:Experimental source: liver
 C:Keywords: glycoprotein; membrane protein

Query Match 25.0%; Score 17; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MTDS 9
 :| |:
 Db 5 LTDS 8

RESULT 8
 GNROL
 leucosulfakinin - Madetra cockroach
 N:Alternate names: LSK
 C:Species: Leucophaea maderae (Madetra cockroach)
 C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996
 C:Accession: A01622
 R:Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
 Science 234, 71-73, 1986
 A:Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and
 A:Reference number: A01622; MUID:86315858
 A:Accession: A01622
 A:Molecule type: protein
 A:Residues: 1-11 <NAC>
 C:Superfamily: gastrin
 C:Keywords: amidated carboxyl end; hormone; sulfoprotein

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:49:13 ; Search time 10.16 Seconds

(without alignments)
45.732 Million cell updates/sec

Title: US-09-780-035-3

Perfect score: 68

Sequence: 1 PLFEDMTSDCR 12

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 463

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	30.9	12	1 PA21_MICFM	P25072 micrurus fu
2	19	27.9	12	1 UR2_SCYCA	P35490 scyllorhinu
3	17	25.0	9	1 UPA3_HUMAN	P30089 homo sapien
4	17	25.0	11	1 LSK1_LEUMA	P04428 leucophaea
5	17	25.0	11	1 PQOC_PSEFL	P55173 pseudomona
6	17	25.0	12	1 V23K_WSSV	P82005 white spot
7	16	23.5	9	1 MOSH_CLYJA	P19853 clypeaster
8	16	23.5	10	1 MOSH_CLYJA	P13358 homo sapien
9	16	23.5	10	1 MOSH_CLYJA	P19662 clypeaster
10	16	23.5	10	1 MOSH_CLYJA	P04558 catostomus
11	16	23.5	12	1 UR2A_CATCO	P01147 gillitchthys
12	16	23.5	12	1 UR2A_CATCO	P13071 ciltrobacter
13	16	23.5	12	1 UR2A_CATCO	P13737 mytilus edu
14	15	22.1	6	1 CIP1_MYTED	P83047 conus ventr
15	15	22.1	6	1 CIP1_MYTED	P83047 conus ventr
16	15	22.1	10	1 NEMS_DROME	P41454 drosophila
17	15	22.1	10	1 NEMS_DROME	P19851 gallus gall
18	15	22.1	10	1 TKNB_CHICK	P01292 sus scrofa
19	15	22.1	11	1 TKNB_CHICK	P82091 littoria cit
20	15	22.1	11	1 CA41_LITCI	P82092 littoria cit
21	15	22.1	11	1 CA41_LITCI	P08611 kassina sen
22	15	22.1	12	1 TKN_KASSE	P81022 polyodon sp
23	15	22.1	12	1 UR2_POLSP	P80709 carlinus ma
24	14	20.6	8	1 ACT_CARMA	P82157 cydia pomon
25	14	20.6	8	1 AL16_CYPDO	P80159 treponema h
26	14	20.6	9	1 FLA2_TREHY	P42993 cyprinus ca
27	14	20.6	9	1 ISOT_CYPCA	P41492 sarcophaga
28	14	20.6	9	1 NSK1_SARBU	P42994 raja clavac
29	14	20.6	9	1 OXYT_RACCL	P40929 homo sapien
30	14	20.6	9	1 UHA2_HUMAN	P41537 ceratotheri
31	14	20.6	10	1 FIBB_CERSI	P30095 homo sapien
32	14	20.6	10	1 UPA9_HUMAN	P36885 periplaneta
33	14	20.6	11	1 LSKP_PERAM	

34	14	20.6	12	1 LICH_BACLI	P82907 bacillus li
35	14	20.6	12	1 TKN2_KASMA	P08614 kassina mac
36	14	20.6	12	1 UR2B_CATCO	P04559 catostomus
37	14	20.6	12	1 YZPY_SCOLI	P17776 escherichia
38	13	19.1	8	1 PLP_BRANA	P81707 brassica na
39	13	19.1	10	1 COXA_ONCMY	P80328 oncorhynch
40	13	19.1	10	1 FARP_MANSE	P18523 manduca sex
41	13	19.1	10	1 UP11_CAEEL	P55956 caenorhabdi
42	13	19.1	10	1 XYNB_DICB4	P80717 dictyoglomu
43	13	19.1	11	1 COXA_CANFA	P99501 canis fami
44	13	19.1	12	1 CXAL_CONIM	P50983 conus imper
45	13	19.1	12	1 UVAL_MOUSE	P99032 mus musculu

ALIGNMENTS

RESULT 1					
PA21_MICFM	STANDARD;	PRT;	12 AA.		
DT 01-MAY-1992 (Rel. 22, Created)					
DT 01-MAY-1992 (Rel. 22, Last sequence update)					
DT 01-MAR-2002 (Rel. 41, Last annotation update)					
DE Phospholipase A2 isozyme 1 (EC 3.1.1.4) (Phosphatidylcholine					
DE 2-acylglycerolase) (Fragment).					
OS Micrurus fulvius microgalbneus (Mexican coral snake).					
OC Lepidosauria; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Eukaryota; Metazoa; Squamata; Scleroglossa; Serpentes; Colubroidae;					
OC Elapidae; Elapinae; Micrurus.					
OX NCBI_TaxID=6536;					
RN [1]					
RP SOURCE.					
RC TISSUE=Venom;					
RA MEDLINE=79255521; PubMed=475771;					
RX Possani L.D., Alagon A.C., Fletcher P.L. Jr., Varela M.J., Julia J.Z.;					
RT Purification and characterization of a phospholipase A2 from the					
RT venom of the coral snake, Micrurus fulvius microgalbneus (Brown and					
RT Smith). J. 179:603-606(1979).					
RL Biochem. J. 179:603-606(1979).					
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE					
CC -2- ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.					
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-					
CC acylglycerophosphocholine + a fatty acid anion.					
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).					
CC -1- SUBCELLULAR LOCATION: Secreted.					
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.					
DR InterPro: IPR001211; PLP_A2.					
DR PROSITE: PS00118; PA2_HIS; PARTIAL.					
DR PROSITE: PS00119; PA2_ASP; PARTIAL.					
KW Hydrolase; Lipid degradation; Calcium; Venom.					
KW NON_TER					
FT					
SQ SEQUENCE 12 AA; 1398 MW; CC21992A89F0339 CRC64;					
Query Match	30.9%	Score 21;	DB 1;	Length 12;	
Best Local Similarity	42.9%	Pred. No. 4.7e+02;			
Matches 3;	Conservative 3;	Mismatches 1;	Indels 0;	Gaps 0;	
QY 3 FEDMTDS 9					
Db 5 FRKMIES 11					
RESULT 2					
UR2_SCYCA	STANDARD;	PRT;	12 AA.		
AC P35490;					
DT 01-JUN-1994 (Rel. 29, Created)					
DT 01-JUN-1994 (Rel. 29, Last sequence update)					
DT 16-OCT-2001 (Rel. 40, Last annotation update)					
DE Urolosteus ii (U-II) (UII).					
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).					

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeidae; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Spinal cord;
 RX MEDLINE=92319231; PubMed=1620290;
 RA Conlon J.M., O'Harte F., Smith D.D., Balment R.J., Hazon N.;
 RT "Purification and characterization of urotensin II and parvalbumin
 from an elasmobranch fish, Scyliorhinus canicula (common dogfish).";
 RL Neuroendocrinology 55:230-235(1992).
 CC -1- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
 CC MUSCLE STIMULATION.
 CC -1- SIMILARITY: BELONGS TO THE UROENSIN 2 FAMILY.
 DR InterPro: IPR001483; Urotensin_II.
 DR Pfam: PF02083; Urotensin_II; 1.
 DR PROSITE: PS00984; UROENSIN_II; 1.
 KW Hormone.
 FT DISULFID
 SQ SEQUENCE 12 AA; 1526 MW; 804729FD579CEBA CRC64;

Query Match 27.9%; Score 19; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 SDC 11
 |||
 DB 4 SDC 6

RESULT 3
 UP33_HUMAN STANDARD; PRT; 9 AA.
 AC P30089;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Fritiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
 DR SWISS-2DPAGE: P30089; HUMAN.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1056 MW; 26F2BBAF769C737 CRC64;

Query Match 25.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PLF 3
 |||
 DB 2 PLF 4

RESULT 4
 LSK1_LEUMA

ID LSK1_LEUMA STANDARD; PRT; 11 AA.
 AC P04428;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Leucosulfakinin-1 (LSK-1).
 OS Leucophaea maderae (Maderia cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86315858; PubMed=3749893;
 RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
 RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
 RT gastrin and cholecystokinin.";
 RL Science 234:71-73(1986).
 CC -1- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF
 CC THE COCKROACH HINDGUT. INHIBITS MUSCLE CONTRACTION OF HINDGUT.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR InterPro: IPR01651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; 1.
 KW Hormone; Amidation; Sulfation.
 FT MOD_RES 6 6
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E8B5AAB CRC64;

Query Match 25.0%; Score 17; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 FED 5
 |||
 DB 3 FED 5

RESULT 5
 PQOC_PSEFL STANDARD; PRT; 11 AA.
 AC P55173;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Coenzyme PQQ synthesis protein C (Fragment).
 GN PQOC.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHA0;
 RX MEDLINE=96064397; PubMed=8526497;
 RA Schnider U., Keel C., Defago G., Haas D.;
 RT "Tn5-directed cloning of pqg genes from Pseudomonas fluorescens CHA0;
 RT mutational inactivation of the genes results in overproduction of the
 RT antibiotic pyoluteorin.";
 RL Appl. Environ. Microbiol. 61:3856-3864(1995).
 CC -1- FUNCTION: REQUIRED FOR COENZYME PYROLO-QUINOLINE-QUINONE (PQQ)
 CC BIOSYNTHESIS.
 CC -1- SIMILARITY: TO OTHER BACTERIAL PQOC.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:48:53 ; Search time 23.8 Seconds
(without alignments)
87.224 Million cell updates/sec

Title: US-09-780-035-3
Perfect score: 68
Sequence: 1 PLFEDMTDSOCR 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 1842

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL.19:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp_invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp Vertebrate:*
15: sp_unclassified:*
16: sp_rvrius:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	32.4	12	6	Q9TRU1	O9trui bos taurus
2	20	29.4	9	2	Q48686	Q48686 lactococcus
3	19	27.9	9	11	Q99JF4	Q99jfa mus musculu
4	19	27.9	10	2	P74843	P74843 streptomyc
5	19	27.9	12	2	Q9WVY6	Q9wvy6 leclercia a
6	19	27.9	12	2	Q9WVY5	Q9wvy5 escherichia
7	19	27.9	12	2	Q9X628	Q9x628 unidentified
8	19	27.9	12	2	Q9X631	Q9x631 pseudomonas
9	19	27.9	12	2	Q9X633	Q9x633 serratia ma
10	19	27.9	12	2	Q9X638	Q9x638 unidentified
11	19	27.9	12	2	Q9X640	Q9x640 citrobacter
12	19	27.9	12	2	Q9X643	Q9x643 klebsiella
13	19	27.9	12	2	Q9X645	Q9x645 unidentified
14	18	26.5	11	7	Q9K332	Q9k332 staphylococ
15	18	26.5	11	7	Q77908	Q77908 oreochromis
16	18	26.5	12	7	Q77877	Q77877 oreochromis

17	18	26.5	12	7	077878	077878 oreochromis
18	18	26.5	12	7	077881	077881 oreochromis
19	18	26.5	12	7	077882	077882 oreochromis
20	18	26.5	12	7	077909	077909 oreochromis
21	18	26.5	12	10	Q9FSA9	Q9fsa9 silene aega
22	17	25.0	10	4	Q9UCR0	Q9ucr0 homo sapien
23	17	25.0	10	10	Q9ES93	Q9es93 silene pent
24	17	25.0	10	10	P82937	P82937 hordium vul
25	17	25.0	11	11	Q9QVH3	Q9qvH3 ratus sp.
26	17	25.0	11	11	Q99N81	Q99n81 mus musculu
27	16	23.5	8	2	Q9R3X0	Q9r3x0 planktothri
28	16	23.5	8	11	Q99NX9	Q99nx9 hydraochoru
29	16	23.5	10	5	Q9TWX1	Q9twx1 dermatophag
30	16	23.5	10	5	P82384	P82384 drosophila
31	16	23.5	10	11	Q9QVK7	Q9qvK7 mus sp. mep
32	16	23.5	11	2	Q47569	Q47569 escherichia
33	16	23.5	11	4	Q9UNL8	Q9unl8 homo sapien
34	16	23.5	11	11	Q99JC3	Q99jc3 ratus sp.
35	16	23.5	12	4	Q9UEH4	Q9ueh4 homo sapien
36	16	23.5	12	4	Q9BYT9	Q9byt9 homo sapien
37	16	23.5	12	6	Q9TR09	Q9tr09 bos taurus
38	16	23.5	12	6	Q9BFW0	Q9bfw0 macropus eu
39	16	23.5	12	6	Q9BFV9	Q9bfv9 choleopus h
40	16	23.5	12	6	Q9BFV8	Q9bfv8 choleopus d
41	16	23.5	12	6	Q9BFV7	Q9bfv7 euphractus
42	16	23.5	12	6	Q9BFV6	Q9bfv6 chaetophrac
43	16	23.5	12	6	Q9BFV5	Q9bfv5 lamandua te
44	16	23.5	12	6	Q9BFV4	Q9bfv4 myrmecophag
45	16	23.5	12	6	Q9BFV3	Q9bfv3 erinaceus c

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	12 AA.
Q9TRU1			
AC Q9TRU1	01-MAY-2000 (TREMBLREL. 13, Created)		
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)			
DT 01-MAY-2000 (TREMBLREL. 13, Last annotation update)			
DE 43 KDA CYANOCEN BROMIDE FRAGMENT PEAK 7.			
OS Bos taurus (Bovine)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC Bovidae; Bovinae; Bos.			
OX NCBI_TaxID=9913;			
RN [1]			
RP SEQUENCE.			
RX MEDLINE=921332498; PubMed=1734497;			
RA Velby O.P., Sletten K., Husby G., Nordstoga K.;			
RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils			
RT of bovine kidney.";			
RL Scand. J. Immunol. 35:63-69(1992).			
SQ SEQUENCE 12 AA; 1257 MW; 0D5C94FDE9B76AA4 CRC64;			

Query Match	32.4%	Score 22;	DB 6;	Length 12;
Best Local Similarity	55.6%	Pred. No. 1.3e+03;		
Matches 5;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY 1 PLFEDMTDS 9				
DB 2 PLFNDPTVS 10				
RESULT 2				
Q48686	PRELIMINARY:	PRT:	9 AA.	
AC Q48686;				
DT 01-NOV-1996 (TREMBLREL. 01, Created)				
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)				
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)				

```

DE STREPTOCOCCUS CREMORIS PROMOTER 23 DNA (FRAGMENT).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8105390; PubMed=2447829;
RA van der Vossen J.M., van der Lelie D., Venema G.;
RT "Isolation and characterization of Streptococcus cremoris Wg2-specific
RT promoters."
RL Appl. Environ. Microbiol. 53:2452-2457(1987).
DR EMBL; M24763; AAA74720.1; -.
FT NON-TER 9
SQ SEQUENCE 9 AA; 1080 MW; 5AF3A44AA469443 CRC64;

Query Match 29.4%; Score 20; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 5.6e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 EDMDTSD 10
Db 2 KNMNDND 8

RESULT 3
09JUF4 PRELIMINARY; PRT; 9 AA.
AC 09JUF4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE OCT-1L (FRAGMENT).
GN OCT-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Pankratova E.V., Deyev I.E., Zhenjlo S.V., Polanovsky O.L.;
RT "Tissue-specific Oct-1 isoforms from murine lymphocytes."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ310124; CAC34946.1; -.
FT NON-TER 9
SQ SEQUENCE 9 AA; 998 MW; 540BCEBABS5BEBA7 CRC64;

Query Match 27.9%; Score 19; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SDC 11
Db 5 SDC 7

RESULT 4
P74843 PRELIMINARY; PRT; 10 AA.
ID P74843;
AC P74843;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-FEB-2001 (TREMBLrel. 19, Last annotation update)
DE CARBOMYCIN RESISTANCE DETERMINANT (FRAGMENT).
GN CARB.
OS Streptomyces thermotolerans.
OC Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=80858;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=TH475;
RA Arita A.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TH475;
RX MEDLINE=8724811; PubMed=3036668;
RA Epp J.K., Burgett S.G., Schoner B.E.;
RT "Cloning and nucleotide sequence of a carbomycin-resistance gene from
RT Streptomyces thermotolerans."
RL Gene 53:73-83(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=TH475;
RX MEDLINE=90185202; PubMed=2628170;
RA Epp J.K., Huber M.L., Turner J.R., Goodson T., Schoner B.E.;
RT "Production of a hybrid macrocyclic antibiotic in Streptomyces
RT amofaciens and Streptomyces lividans by introduction of a cloned
RT carbomycin biosynthetic gene from Streptomyces thermotolerans."
RL Gene 85:293-301(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=TH475;
RX MEDLINE=94122440; PubMed=7764361;
RA Arita A., Kawamura N., Tsunekawa H., Okamura K., Tone H.,
RA Okamoto R.;
RT "Cloning and nucleotide sequences of two genes involved in the 4'-O-
RT acylation of macrolide antibiotics from Streptomyces thermotolerans."
RL Biosci. Biotechnol. Biochem. 57:2020-2025(1993).
DR EMBL; D31821; BAA06606.1; -.
FT NON-TER 1
SQ SEQUENCE 10 AA; 1214 MW; 58565CE72B1B19C7 CRC64;

Query Match 27.9%; Score 19; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEEDM 6
Db 3 LEEDL 7

RESULT 5
09WYV6 PRELIMINARY; PRT; 12 AA.
ID 09WYV6;
AC 09WYV6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE MERR (FRAGMENT).
GN MERR.
OS Leclercia adecarboxylata.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Leclercia.
OX NCBI_TaxID=83655;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=665H, 533H, 742H, AND 505H;
RX MEDLINE=97208220; PubMed=9055422;
RA Liebert C.A., Wieman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RT bacteria isolated from the fecal flora of primates."
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=665H, 533H, 742H, AND 505H;
RX MEDLINE=98027386; PubMed=9361435;
RA Wieman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RT gram-negative fecal bacteria of primates."
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:53 ; Search time 29.25 Seconds
(without alignments)
45.569 Million cell updates/sec

Title: US-09-780-035-3
Perfect score: 68
Sequence: 1 PLFEDMTSDSCR 12

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 158732

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
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17:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
18:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
21:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*
22:	/SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	12	22	AA65293
2	33	48.5	6	19	AAW77073
3	33	48.5	6	19	AAW48957
4	30	44.1	9	22	AA684433
5	28	41.2	10	18	AAW09939
6	28	41.2	10	22	AA685374
7	27	39.7	11	15	AA60024
8	27	39.7	11	15	AA684547
9	26	38.2	9	22	AA688741
10	26	38.2	10	22	AAU25766
11	26	38.2	12	19	AAW56757

12	26	38.2	12	20	AA94419	Plasmodium falciparum
13	26	38.2	12	22	AB32222	Human APL-176 tryp
14	26	38.2	12	22	AAU28440	DPI tryptic digest
15	26	38.2	12	22	AAU28470	DPI tryptic digest
16	26	38.2	12	22	AAU24807	Schizophrenia-Asso
17	26	38.2	12	22	AAU24873	Schizophrenia-Asso
18	26	38.2	12	22	AAU25019	Schizophrenia-Asso
19	26	38.2	12	22	AAU25387	Schizophrenia-Asso
20	26	38.2	12	22	AAU26086	Depression-Asso
21	26	38.2	12	22	AAU26116	Depression-Asso
22	26	38.2	12	22	AAU15151	Schizophrenia-Asso
23	26	38.2	12	22	AAU15217	Schizophrenia-Asso
24	26	38.2	12	22	AAU15363	Schizophrenia-Asso
25	26	38.2	12	22	AAU15731	Schizophrenia-Asso
26	26	36.8	7	15	AA65642	Peptide displaying
27	25	36.8	9	18	AAW10281	Antibody ACA-6626
28	25	36.8	9	19	AAW67137	Antiphospholipid a
29	25	36.8	9	19	AAW46072	Antiphospholipid a
30	25	36.8	9	21	AAV32443	Integrin alpha-v b
31	25	36.8	10	22	AA684332	Arabidopsis thaliana
32	25	36.8	12	9	AA681900	Organ specific neo
33	25	36.8	12	12	AA610696	Human lactate dehy
34	24	35.3	8	22	AAE06012	Zinc finger protein
35	24	35.3	8	22	AAE02076	Murine zlf268 flng
36	24	35.3	10	20	AAV23721	Peptide identified
37	24	35.3	10	21	AA601352	Functional fragmen
38	24	35.3	10	22	AA694896	Human complementar
39	24	35.3	11	21	AAV90159	UPAR targeting seq
40	24	35.3	12	18	AAW34113	LFA-1 alpha subuni
41	24	35.3	12	18	AAW34110	LFA-1 alpha subuni
42	24	35.3	12	18	AAW36724	Thrombopoietin rec
43	24	35.3	12	21	AAW09573	Thrombopoietin rec
44	24	35.3	12	18	AAV51054	Ecodnapoli derived
45	24	35.3	12	22	AAU25943	Human thrombopoiet

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description
1	AA65293	68	100.0	12	22	AA65293
2	AA65293	33	48.5	6	19	AAW77073
3	AA65293	33	48.5	6	19	AAW48957
4	AA65293	30	44.1	9	22	AA684433
5	AA65293	28	41.2	10	18	AAW09939
6	AA65293	28	41.2	10	22	AA685374
7	AA65293	27	39.7	11	15	AA60024
8	AA65293	27	39.7	11	15	AA684547
9	AA65293	26	38.2	9	22	AA688741
10	AA65293	26	38.2	10	22	AAU25766
11	AA65293	26	38.2	12	19	AAW56757

Human interleukin-18 (IL-18) peptide epitope.

IL-18: interleukin-18; human; antibody; antitumor; antiparasitic; antipneumatic; cerebroprotective; neurotrophic; neurological; antinflammatory; antiparkinsonian; cardiant; immunosuppressive; antidepressant; neuroleptic; hepatotropic.

Homo sapiens.

WO200158956-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US04170.

10-FEB-2000; 2000US-0181608.

(BADI) BASF AG.

Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfield J; Duncan AR, Brocklehurst SM, Mankovich J, Shorrocks CP, Thompson JB; Lennard SN; WPI: 2001-550020/61.

Novel antibodies and compounds capable of binding to human interleukin-18 useful for treating, e.g., inflammatory disorders.

PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Claim 11; Page 70; 91pp; English.
 XX
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 peptide epitope.
 XX
 SO Sequence 12 AA;
 XX
 OY 1 PFEDMTDSDCR 12
 DB 1 plfedmtsdscr 12
 XX
 RESULT 2
 AAM77073
 ID AAM77073 standard; peptide; 6 AA.
 XX
 AC AAM77073;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE Human interleukin 18 peptide 2.
 XX
 KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity ositis; primary hyperthyroidism.
 XX
 OS Homo sapiens.
 XX
 PN EP861663-A2.
 XX
 PD 02-SEP-1998.
 XX
 PF 24-FEB-1998; 98EP-0301352.
 XX
 PR 25-FEB-1997; 97JP-0055468.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
 XX
 DR WPI; 1998-448964/39.
 XX
 CC Use of interleukin-18 to inhibit osteoclast formation - in treatment
 CC of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 CC osteosarcoma, chronic rheumatoid arthritis, deformity ositis,
 CC primary hyperthyroidism and osteoporosis
 CC
 CC Claim 2; Page 17; 56pp; English.
 CC
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma

CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity ositis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SO Sequence 6 AA;
 XX
 OY 3 FEDMTD 8
 DB 1 fedmtd 6
 XX
 Query Match 48.5%; Score 33; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 RESULT 3
 AAM48957
 ID AAM48957 standard; Peptide; 6 AA.
 XX
 AC AAM48957;
 XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Consensus sequence 2 present in interferon-gamma inducing factor.
 XX
 KW Interferon-gamma inducing factor; interferon-gamma; Killer cell;
 KW antitumor agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome;
 XX
 OS Homo sapiens.
 XX
 PN EP845530-A2.
 XX
 PD 03-JUN-1998.
 XX
 PF 28-NOV-1997; 97EP-0309632.
 XX
 PR 14-NOV-1997; 97JP-0329715.
 PR 29-NOV-1996; 96JP-0333037.
 PR 21-JAN-1997; 97JP-0020906.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Kurimoto M, Okamoto I, Yamamoto K;
 XX
 DR WPI; 1998-288747/26.
 XX
 CC Mutants of interferon-gamma inducing polypeptide - useful as
 CC antitumour, antiviral, antimicrobial or anti-immunopathic agents
 CC
 CC Claim 1; page 39; 59pp; English.
 CC
 CC The present claimed consensus sequence is present in the human
 CC (AAM48957) and mouse (AAM48960) interferon-gamma inducing factor (IGIF).
 CC The invention provides for mutant human and mouse interferon-gamma
 CC inducing factors in which one or more cysteine residues are replaced
 CC with different residues at or away from the consensus sequences shown
 CC in AAM48956-W48958. The mutant IGIFs are capable of stimulating
 CC immunocompetent cells for the production of interferon-gamma and are
 CC claimed to be less toxic, more active and stable than the corresponding
 CC wild type IGIF. The mutant IGIFs are also claimed to enhance killer
 CC cell cytotoxicity and/or induce killer cell formation, and may therefore
 CC be useful as antitumour agents, antitumour immunotherapeutics, antiviral
 CC agents and antimicrobial agents. The mutant IGIFs are also claimed to
 CC be useful for treating hepatitis, acquired immunodeficiency syndrome
 CC (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal
 CC carcinoma), rheumatism, osteoporosis and thrombopenia caused by
 CC radiation- and chemo-therapy.
 XX

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:25:33 ; Search time 12.85 Seconds

(without alignments)
22.810 Million cell updates/sec

Title: US-09-780-035-3

Perfect score: 68

Sequence: 1 PLFEDMTSDCR 12

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 83765

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	39.7	11	1 US-08-455-559-4	Sequence 4, Appl
2	27	39.7	11	1 US-08-481-377-4	Sequence 4, Appl
3	27	39.7	11	3 US-09-153-733A-4	Sequence 4, Appl
4	27	39.7	11	4 US-09-145-060-4	Sequence 4, Appl
5	27	39.7	11	5 PCT-US94-00657-4	Sequence 4, Appl
6	27	39.7	11	5 PCT-US94-00666-4	Sequence 4, Appl
7	26	38.2	8	4 US-09-288-061-1	Sequence 1, Appl
8	26	38.2	12	1 US-08-796-772A-1	Sequence 1, Appl
9	25	36.8	7	1 US-08-248-538-17	Sequence 17, Appl
10	25	36.8	9	2 US-08-690-605-18	Sequence 18, Appl
11	25	36.8	9	2 US-08-482-651-47	Sequence 47, Appl
12	25	36.8	9	4 US-08-660-092-50	Sequence 50, Appl
13	25	36.8	10	1 US-07-750-278-3	Sequence 31, Appl
14	25	36.8	10	1 US-08-090-193-31	Sequence 31, Appl
15	25	36.8	10	2 US-08-486-569-31	Sequence 31, Appl
16	25	36.8	10	2 US-08-488-027-31	Sequence 31, Appl
17	25	36.8	10	2 US-08-090-192-31	Sequence 31, Appl
18	25	36.8	10	2 US-08-482-663-31	Sequence 31, Appl
19	25	36.8	10	2 US-08-482-658-31	Sequence 31, Appl
20	25	36.8	10	3 US-08-470-349-31	Sequence 31, Appl
21	25	36.8	10	3 US-08-475-610-31	Sequence 31, Appl
22	25	36.8	10	5 PCT-US92-00277-31	Sequence 31, Appl
23	25	36.8	10	5 PCT-US92-00278-31	Sequence 31, Appl
24	25	35.3	5	2 US-08-404-531B-42	Sequence 42, Appl
25	24	35.3	5	2 US-08-476-900A-42	Sequence 42, Appl
26	24	35.3	5	3 US-08-488-546A-42	Sequence 42, Appl
27	24	35.3	5	3 US-08-488-546A-42	Sequence 42, Appl

28	24	35.3	10	2 US-08-902-623-67	Sequence 67, Appl
29	24	35.3	12	2 US-08-764-640-129	Sequence 129, Appl
30	24	35.3	12	3 US-08-844-978-16	Sequence 16, Appl
31	24	35.3	12	3 US-08-844-978-19	Sequence 19, Appl
32	24	35.3	12	3 US-08-973-225-129	Sequence 129, Appl
33	24	35.3	12	3 US-09-244-296A-129	Sequence 129, Appl
34	24	35.3	12	4 US-09-516-704-129	Sequence 129, Appl
35	23	33.8	9	4 US-08-392-459-36	Sequence 36, Appl
36	23	33.8	9	5 PCT-US91-08525-36	Sequence 36, Appl
37	23	33.8	5	4 US-09-187-859-2333	Sequence 2333, Appl
38	22	32.4	5	4 US-09-187-859-3587	Sequence 3587, Appl
39	22	32.4	6	4 US-09-187-859-2336	Sequence 2336, Appl
40	22	32.4	6	4 US-09-187-859-3591	Sequence 3591, Appl
41	22	32.4	7	4 US-09-187-859-2339	Sequence 2339, Appl
42	22	32.4	7	4 US-09-187-859-3593	Sequence 3593, Appl
43	22	32.4	8	4 US-09-187-859-2242	Sequence 2242, Appl
44	22	32.4	8	4 US-09-187-859-2242	Sequence 2242, Appl
45	22	32.4	8	4 US-09-187-859-2242	Sequence 2242, Appl

ALIGNMENTS

RESULT 1
US-08-455-559-4
Sequence 4, Application US/08455559
Patent No. 5801014
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HOYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERILL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD2280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 121
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
US-08-455-559-4

Query Match 39.7%; Score 27; DB 1; Length 11;
Best Local Similarity 44.4%; Pred. No. 81;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 FEDMTSDC 11
:111:1
Db 1 YEDMVVDEC 9

RESULT 2
US-08-481-377-4
; Sequence 4, Application US/08481377
; Patent No. 5808007
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,377
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00666
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: SJL121
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
US-08-481-377-4

Query Match 39.7%; Score 27; DB 1; Length 11;
Best Local Similarity 44.4%; Pred. No. 81;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 FEDMTSDC 11
:111:1
Db 1 YEDMVVDEC 9

RESULT 3
US-09-153-733A-4
; Sequence 4, Application US/09153733A
; Patent No. 6025475
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/153,733A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/481,377
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: SJL121
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
US-09-153-733A-4

Query Match 39.7%; Score 27; DB 3; Length 11;
Best Local Similarity 44.4%; Pred. No. 81;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 FEDMTSDC 11
:111:1
Db 1 YEDMVVDEC 9

RESULT 4
US-09-145-060-4
; Sequence 4, Application US/09145060
; Patent No. 6245896
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-jin
; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0

PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 XX
 PS Claim 11; Page 13; 91pp; English.
 XX
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 peptide epitope.
 XX
 SQ Sequence 14 AA:
 QY 1 VIRINDQVLFIDQ 14
 Db 1 virindqvlfidq 14
 Query Match 100.0%; Score 69; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 AAG65324
 ID AAG65324 standard; peptide; 14 AA.
 AC AAG65324;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) peptide epitope.
 XX
 KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI; 2001-550020/61.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Example 1; Page 13; 91pp; English.
 CC The invention provides isolated antibodies, or antigen-binding portions,

CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents a human IL-18 peptide epitope.
 XX
 SQ Sequence 14 AA:
 QY 6 NDQVLFIDQ 14
 Db 1 ndqvlfidq 9
 Query Match 66.7%; Score 46; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 AAG65322
 ID AAG65322 standard; peptide; 14 AA.
 AC AAG65322;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human interleukin-18 (IL-18) peptide epitope.
 XX
 KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI; 2001-550020/61.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Example 1; Page 13; 91pp; English.
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and

CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrently, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents a human IL-18 peptide epitope.
XX
SQ Sequence 14 AA;

Query Match 63.8%; Score 44; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIRINDQV 9
|:|||||:
Db 6 virnldqv 14

RESULT 4
AAU26762
ID AAU26762 standard; Peptide: 10 AA.
XX
AC AAU26762;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human Leukocyte Antigen (HLA) HLA-A2.1 immunogenic binding peptide #205.
XX
KM Immunogenic peptide; human leukocyte antigen; HLA-A2.1 binding motif;
KW immunostimulant; cytostatic; antiviral; glycoprotein; cytotoxic T cell;
KW viral disease; prostate cancer; hepatitis B; hepatitis C; lymphoma; AIDS;
KW renal carcinoma; cervical carcinoma; condyloma acuminatum.
XX
XX Homo sapiens.
OS
PN WO200162776-A1.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2000; 2000WO-US04655.
XX
PR 23-FEB-2000; 2000WO-US04655.
XX
PA (EPTM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Kast WM, Southwood S;
XX
DR WPI: 2001-582039/65.
XX
PT Composition for treating viral diseases and cancer comprises an
XX immunogenic peptide having an HLA-A2.1 binding motif -
XX
PS Example 1; Page 34; 85pp; English.
XX
CC Sequences AAU26558-AAU27161 represent immunogenic peptides containing a
CC human leukocyte antigen A2.1 (HLA-A2.1) binding motif. The peptides of
CC the invention are capable of specifically binding glycoproteins encoded
CC by HLA alleles and inducing a cytotoxic T cell response against an
CC antigen in a patient expressing HLA-A2.1. This method is useful for the
CC treatment, prevention and diagnosis of pathological states such as viral
CC diseases and cancers, including prostate cancer, hepatitis B,
CC hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and
CC condyloma acuminatum. The peptides are used for treatment of chronic
CC infection and for stimulating the immune system to eliminate
CC virus-infected cells.
XX
SQ Sequence 10 AA;

Query Match 47.8%; Score 33; DB 22; Length 10;

Best Local Similarity 50.0%; Pred. No. 9.6;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 RNLNDQVLEI 12
|:|||||:
Db 1 rnmndqlmf1 10

RESULT 5
AAU27095
ID AAU27095 standard; Peptide: 10 AA.
XX
AC AAU27095;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human Leukocyte Antigen (HLA) HLA-A2.1 immunogenic binding peptide #379.
XX
KM Immunogenic peptide; human leukocyte antigen; HLA-A2.1 binding motif;
KW immunostimulant; cytostatic; antiviral; glycoprotein; cytotoxic T cell;
KW viral disease; prostate cancer; hepatitis B; hepatitis C; lymphoma; AIDS;
KW renal carcinoma; cervical carcinoma; condyloma acuminatum.
XX
XX Homo sapiens.
OS
PN WO200162776-A1.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2000; 2000WO-US04655.
XX
PR 23-FEB-2000; 2000WO-US04655.
XX
PA (EPTM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Kast WM, Southwood S;
XX
DR WPI: 2001-582039/65.
XX
PT Composition for treating viral diseases and cancer comprises an
XX immunogenic peptide having an HLA-A2.1 binding motif -
XX
PS Claim 1; Page 72; 85pp; English.
XX
CC Sequences AAU26558-AAU27161 represent immunogenic peptides containing a
CC human leukocyte antigen A2.1 (HLA-A2.1) binding motif. The peptides of
CC the invention are capable of specifically binding glycoproteins encoded
CC by HLA alleles and inducing a cytotoxic T cell response against an
CC antigen in a patient expressing HLA-A2.1. This method is useful for the
CC treatment, prevention and diagnosis of pathological states such as viral
CC diseases and cancers, including prostate cancer, hepatitis B,
CC hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and
CC condyloma acuminatum. The peptides are used for treatment of chronic
CC infection and for stimulating the immune system to eliminate
CC virus-infected cells.
XX
SQ Sequence 10 AA;

Query Match 47.8%; Score 33; DB 22; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.6;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 RNLNDQVLEI 12
|:|||||:
Db 1 rnmndqlmf1 10

RESULT 6
AAU06399
ID AAU06399 standard; Peptide: 10 AA.
XX
AC AAU06399;

XX 24-OCT-2001 (first entry)
 XX Human prostate antigen binding peptide #21.
 DE Prostate cancer-associated antigen; supermotif; human leukocyte antigen;
 KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;
 KM immunogenicity; immunosuppression; HTL.
 XX Homo sapiens.
 OS
 PN WO200145728-A2.
 PD 28-JUN-2001.
 XX 20-DEC-2000; 2000WO-US35516.
 PF 21-DEC-1999; 99US-0171312.
 PR 07-AUG-2000; 2000US-0633364.
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;
 DR WPI; 2001-398311/42.
 XX
 PT Tumour antigen-associated group-based vaccines useful for vaccinating
 PT against prostate cancer -
 PS Example 2; Page 237; 252pp; English.
 XX The sequences represent prostate cancer-associated antigens and derived
 CC motif or supermotif epitopes. The peptide epitopes are included in
 CC prostate cancer vaccine compositions due to their ability to bind to
 CC human leukocyte antigen (HLA) molecules, which recognise the motifs.
 CC peptides with a high binding affinity are further tested for their
 CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte
 CC (HTL) response. Supermotif-bearing peptides may also be tested for their
 CC binding affinity to multiple alleles within the HLA superfamily. The
 CC vaccine compositions can be modified, for example, to enhance
 CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to
 CC alter the immune response to suit the target disease. These group-based
 CC vaccines allow the focus of an immune response to multiple selected
 CC antigens from the same pathogen. Variability among the immune responses
 CC of patients can therefore be alleviated by the inclusion of groups from
 CC multiple antigens in a vaccine.
 CC
 SQ Sequence 10 AA;
 XX
 XX Query Match 47.8%; Score 33; DB 22; Length 10;
 XX Best Local Similarity 50.0%; Pred. No. 9.6;
 XX Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 3 RNINDQVLF1 12
 XX I :|||::|:
 Db 1 rmmndqlmfl 10
 XX
 XX RESULT 7
 XX AAU06459
 ID AAU06459 standard; Peptide; 10 AA.
 XX
 AC AAU06459;
 XX
 XX 24-OCT-2001 (first entry)
 DE Human leukocyte Antigen-A2 (HLA-A2) supermotif binding peptide #51.
 KW Prostate cancer-associated antigen; supermotif; human leukocyte antigen;
 KM HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;
 KW immunogenicity; immunosuppression; HTL.

XX Homo sapiens.
 OS
 PN WO200145728-A2.
 PD 28-JUN-2001.
 XX 20-DEC-2000; 2000WO-US35516.
 PF 21-DEC-1999; 99US-0171312.
 PR 07-AUG-2000; 2000US-0633364.
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;
 DR WPI; 2001-398311/42.
 XX
 PT Tumour antigen-associated group-based vaccines useful for vaccinating
 PT against prostate cancer -
 PS Example 2; Page 240; 252pp; English.
 XX The sequences represent prostate cancer-associated antigens and derived
 CC motif or supermotif epitopes. The peptide epitopes are included in
 CC prostate cancer vaccine compositions due to their ability to bind to
 CC human leukocyte antigen (HLA) molecules, which recognise the motifs.
 CC peptides with a high binding affinity are further tested for their
 CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte
 CC (HTL) response. Supermotif-bearing peptides may also be tested for their
 CC binding affinity to multiple alleles within the HLA superfamily. The
 CC vaccine compositions can be modified, for example, to enhance
 CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to
 CC alter the immune response to suit the target disease. These group-based
 CC vaccines allow the focus of an immune response to multiple selected
 CC antigens from the same pathogen. Variability among the immune responses
 CC of patients can therefore be alleviated by the inclusion of groups from
 CC multiple antigens in a vaccine.
 CC
 SQ Sequence 10 AA;
 XX
 XX Query Match 47.8%; Score 33; DB 22; Length 10;
 XX Best Local Similarity 50.0%; Pred. No. 9.6;
 XX Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 3 RNINDQVLF1 12
 XX I :|||::|:
 Db 1 rmmndqlmfl 10
 XX
 XX RESULT 8
 XX AAU77072
 ID AAU77072 standard; peptide; 6 AA.
 XX
 AC AAU77072;
 XX
 XX 16-NOV-1998 (first entry)
 DE Human interleukin 18 peptide.
 KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteosarcoma; Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity ossitis; primary hyperthyroidism.
 XX
 OS Homo sapiens.
 PN EP861663-A2.
 PD 02-SEP-1998.
 PF 24-FEB-1998; 98EP-0301352.

XX 25-FEB-1997; 97JP-0055468.
 XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
 XX WPI; 1998-448964/39.
 XX
 XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 PT primary hyperthyroidism and osteoporosis
 PS Claim 2; Page 17; 56pp; English.
 XX
 XX Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 XX Sequence 6 AA;

Query Match 44.9%; Score 31; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NDQVLF 11
 |||||
 Db 1 ndqvlf 6

RESULT 9

AAW48956
 ID AAW48956 standard; Peptide; 6 AA.

AC AAW48956;

DT 25-SEP-1998 (first entry)

DE Consensus sequence 1 present in interferon-gamma inducing factor.

KW Interferon-gamma inducing factor; interferon-gamma; killer cell;
 KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome;
 KM consensus.

OS Homo sapiens.
 OS Mus sp.

PN EP845530-A2.

PD 03-JUN-1998.

PE 28-NOV-1997; 97EP-0309632.

PR 14-NOV-1997; 97JP-0329715.

PR 29-NOV-1996; 96JP-0333037.

PR 21-JAN-1997; 97JP-0020906.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Kurimoto M, Okamoto I, Yamamoto K;

DR WPI; 1998-288747/26.

PT Mutants of interferon-gamma inducing polypeptide - useful as
 PT antitumour, antiviral, antimicrobial or anti-immunopathic agents

PS Claim 1; page 39; 59pp; English.
 XX
 XX The present claimed consensus sequence is present in the human
 CC (AAW48956) and mouse (AAW48960) interferon-gamma inducing factor (IGIF).
 CC The invention provides for mutant human and mouse interferon-gamma
 CC inducing factors in which one or more cysteine residues are replaced
 CC with different residues at or away from the consensus sequences shown
 CC in AAW48956-W48958. The mutant IGIFs are capable of stimulating
 CC immunocompetent cells for the production of interferon-gamma and are
 CC claimed to be less toxic, more active and stable than the corresponding
 CC wild type IGIF. The mutant IGIFs are also claimed to enhance killer
 CC cell cytotoxicity and/or induce killer cell formation, and may therefore
 CC be useful as antitumour agents, antitumour immunotherapeutics, antiviral
 CC agents and antimicrobial agents. The mutant IGIFs are also claimed to
 CC be useful for treating hepatitis, acquired immunodeficiency syndrome
 CC (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal
 CC carcinoma), rheumatism, osteoporosis and thrombopenia caused by
 CC radiation- and chemo-therapy.
 XX
 XX Sequence 6 AA;

Query Match 44.9%; Score 31; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NDQVLF 11
 |||||
 Db 1 ndqvlf 6

RESULT 10

AAW09901
 ID AAW09901 standard; Peptide; 9 AA.

AC AAW09901;

DT 16-OCT-1997 (first entry)

DE Prostate specific membrane antigen peptide PSM-P12.

KW Prostate specific membrane antigen; PSMA; prostate specific antigen;
 KW PSA; prostate cancer; adoptive cellular immunotherapy; therapy;
 KW vaccine.

OS Homo sapiens.

PN W09704802-A1.

PD 13-FEB-1997.

PE 29-JUL-1996; 96WO-US12389.

PR 31-JUL-1995; 95US-0509254.

PA (PACT-) PACIFIC NORTHWEST CANCER FOUND.

PI Boynton AL, Murphy GP, Tjoa BA;

DR WPI; 1997-145375/13.

PT Use of dendritic cells for prostate cancer immuno:therapy - the
 PT cells are exposed to prostate cancer antigen, then administered to
 PT the patient where they activate and proliferate T-cells

PS Claim 3; Page 47; 69pp; English.

XX Peptide PSM-P12 (AAW09901) corresponds to amino acid residues 663-701
 CC of prostate specific membrane antigen (PSMA). A method for
 CC producing a cancer growth inhibiting response comprises exposing
 CC human dendritic cells (DCs) to PSM-P12 or other PSMA or prostate
 CC specific antigen peptides (see also AAW09889-900 and AAW09902-26), and
 CC then administering the DCs to a prostate cancer patient to activate

CC T cell responses in vivo. Alternatively, the T cell response is
CC activated in vitro and the T cells are then administered to the
CC patient. In either case, the DCs are used to elicit an
CC immunotherapeutic growth inhibiting response against a primary or
CC metastatic prostate tumour. PSW-P12 was selected to be presented
CC by DCs to activate T cells of a patient which match the A2
CC haplotype.
CC
XX
SQ Sequence 9 AA;

Query Match 43.5%; Score 30; DB 18; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNDQVLEFI 12
Db 2 mndqlmfl 9

RESULT 11
ID AAY82833 standard; peptide; 9 AA.
XX
AC AAY82833;
XX
DT 19-JUN-2000 (first entry)
XX
DE Prostate specific membrane antigen fragment (tumour associated antigen).
XX
XX Tumour associated antigen peptide; TAA; cancer; carcinoma;
XX treatment; prevention; cure; anti-tumour vaccine; metastases;
XX breast; bladder; prostate; pancreas; ovary; thyroid; colon;
XX stomach; carcinoma; MHC Class I; HLA-A2; human;
XX Major Histocompatibility Complex; uroplakin;
XX prostate specific antigen; prostate specific membrane antigen;
XX prostate acid phosphatase; mucin; lactadherin;
XX teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1.
XX
XX Homo sapiens.
XX
OS
XX
PN WO200006723-A1.
XX
PD 10-FEB-2000.
XX
XX
PF 29-JUL-1999; 99WO-IL00417.
XX
XX
PR 30-JUL-1998; 98IL-0125608.
XX
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX (BIOF-) BIO-TECHNOLOGY GEN CORP.
XX
XX
PI Eisenbach L, Carmon L, Tirosh B, Bar-haim E, Paz A, Fridkin M;
PI Filter-atlas C;
XX
DR WPI; 2000-205463/18.
XX
XX
PT Tumour associated antigen peptides, especially derived from uroplakin,
PT useful as vaccines to prevent or cure cancers including breast,
PT bladder, prostate, pancreas, ovary, thyroid, colon and stomach -
XX
XX
XX Claim 8; Page 97; 113pp; English.
XX
XX Tumour associated antigen peptides (TAA) may be used for the
XX treatment, prevention and cure of cancer or cancer metastases. The
XX cancer may be breast, bladder, prostate, pancreas, ovary, thyroid,
XX colon, stomach, head or neck cancer or a carcinoma. The tumour
XX associated antigens are presentable to the immune system by HLA-A2
XX molecules and are generally between 8 to 10 amino acids in length.
XX The amino acids located at positions 2 and 9 of the tumour associated
XX antigens are the anchor residues which participate in the binding to
XX MHC class I molecules, more specifically HLA-A2. More tumour
XX associated antigens are described in GENESEQ records AAY82806-182882.

CC Those tumour associated antigens described in records AAY82806-182824
CC and AAY82855-182869 are derived from Uroplakin, such as Uroplakin II,
CC Uroplakin Ia, Uroplakin III and Uroplakin Ib. Those described in
CC records AAY82825-182829 are derived from prostate specific antigen
CC (PSA). Those described in records AAY82830-182835 are derived from
CC prostate specific membrane antigen (PSMA). Those described in
CC records Y182836-AAY82839 are derived from prostate acid phosphatase
CC (PAP). Those described in records AAY82840-182846 are derived
CC from lactadherin (BA-46). Those described in records AAY82847-182854
CC are derived from Mucin and those described in records AAY82871-182882
CC are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
CC
XX
SQ Sequence 9 AA;

Query Match 43.5%; Score 30; DB 21; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNDQVLEFI 12
Db 2 mndqlmfl 9

RESULT 12
ID AAU09108 standard; Peptide; 9 AA.
XX
AC AAU09108;
XX
DT 16-JAN-2002 (first entry)
XX
XX Human PSMA derived immunogenic peptide CLP336.
XX
DE Human PSMA derived immunogenic peptide CLP336.
XX
XX Human; PSMA; prostate specific membrane antigen; prostate cancer;
XX tumour; Immunogenic peptide; cytostatic; immunogen; CLP336.
XX
XX
XX Homo sapiens.
XX
OS
XX
PN WO200174845-A2.
XX
XX
PD 11-OCT-2001.
XX
XX
PF 30-MAR-2001; 2001WO-CA00411.
XX
XX
PR 31-MAR-2000; 2000US-193386P.
XX
XX
PA (AVET) AVENTIS PASTEUR LTD.
XX
XX
PI Pedyczak A, Chong P, Sia CDY;
PI WPI; 2001-626378/72.
XX
DR N-PSDB; AAS15143.
XX
XX
XX New polypeptides useful for inducing an immune response and treating
XX prostate cancer comprises polypeptides derived from the prostate
XX specific membrane antigen -
XX
XX
PS Claim 2; Page 34; 47pp; English.
XX
XX
XX The invention relates to prostate specific membrane antigen (PSMA)
XX derived peptides (and the nucleic acids encoding them) capable of
XX eliciting an immune response. The molecules of the invention are used to
XX elicit an immune response, particularly to treat cancer and tumours,
XX especially prostate cancer. Delivery of the peptides may be by
XX expression from the nucleic acids encoding them (i.e. gene therapy).
XX The present sequence represents a PSMA derived immunogenic peptide
XX representing amino acids 663-671 of PSMA.
XX
SQ Sequence 9 AA;

Query Match 43.5%; Score 30; DB 22; Length 9;

Best Local Similarity 50.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNDQVLEI 12
:||||:|
Db 2 mndqlmfl 9

RESULT 13
AAU26758
ID AAU26758 standard; Peptide; 9 AA.
XX
AC AAU26758;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human Leukocyte Antigen (HLA) HLA-A2.1 immunogenic binding peptide #201.
XX
KW Immunogenic peptide; human leukocyte antigen: HLA-A2.1 binding motif;
KW immunostimulant; cytostatic; antiviral; glycoprotein; cytotoxic T cell;
KW viral disease; prostate cancer; hepatitis B; hepatitis C; lymphoma; AIDS;
KW renal carcinoma; cervical carcinoma; condyloma acuminatum.
XX
OS Homo sapiens.
XX
PI WO200162776-A1.
XX
PN 30-AUG-2001.
XX
PD 23-FEB-2000; 2000WO-US04655.
XX
PF 23-FEB-2000; 2000WO-US04655.
XX
PR 23-FEB-2000; 2000WO-US04655.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Kast WM, Southwood S;
XX
DR WPI; 2001-582039/65.
XX
PT Composition for treating viral diseases and cancer comprises an
XX immunogenic peptide having an HLA-A2.1 binding motif -
XX
PS Example 1; Page 34; 85pp; English.
XX
CC Sequences AAU26558-AAU27161 represent immunogenic peptides containing a
CC human leukocyte antigen A2.1 (HLA-A2.1) binding motif. The peptides of
CC the invention are capable of specifically binding glycoproteins encoded
CC by HLA alleles and inducing a cytotoxic T cell response against an
CC antigen in a patient expressing HLA-A2.1. This method is useful for the
CC treatment, prevention and diagnosis of pathological states such as viral
CC diseases and cancers, including prostate cancer, hepatitis B,
CC hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and
CC condyloma acuminatum. The peptides are used for treatment of chronic
CC infection and for stimulating the immune system to eliminate
CC virus-infected cells.
XX
SQ Sequence 9 AA;

Query Match 43.5%; Score 30; DB 22; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNDQVLEI 12
:||||:|
Db 2 mndqlmfl 9

RESULT 14
AAU27091
ID AAU27091 standard; Peptide; 9 AA.
XX
AC AAU27091;

XX 18-DEC-2001 (first entry)
DT
XX
DE Human Leukocyte Antigen (HLA) HLA-A2.1 immunogenic binding peptide #375.
XX
KW Immunogenic peptide; human leukocyte antigen: HLA-A2.1 binding motif;
KW immunostimulant; cytostatic; antiviral; glycoprotein; cytotoxic T cell;
KW viral disease; prostate cancer; hepatitis B; hepatitis C; lymphoma; AIDS;
KW renal carcinoma; cervical carcinoma; condyloma acuminatum.
XX
OS Homo sapiens.
XX
PI WO200162776-A1.
XX
PN 30-AUG-2001.
XX
PD 23-FEB-2000; 2000WO-US04655.
XX
PF 23-FEB-2000; 2000WO-US04655.
XX
PR 23-FEB-2000; 2000WO-US04655.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Kast WM, Southwood S;
XX
DR WPI; 2001-582039/65.
XX
PT Composition for treating viral diseases and cancer comprises an
XX immunogenic peptide having an HLA-A2.1 binding motif -
XX
PS Claim 1; Page 71; 85pp; English.
XX
CC Sequences AAU26558-AAU27161 represent immunogenic peptides containing a
CC human leukocyte antigen A2.1 (HLA-A2.1) binding motif. The peptides of
CC the invention are capable of specifically binding glycoproteins encoded
CC by HLA alleles and inducing a cytotoxic T cell response against an
CC antigen in a patient expressing HLA-A2.1. This method is useful for the
CC treatment, prevention and diagnosis of pathological states such as viral
CC diseases and cancers, including prostate cancer, hepatitis B,
CC hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and
CC condyloma acuminatum. The peptides are used for treatment of chronic
CC infection and for stimulating the immune system to eliminate
CC virus-infected cells.
XX
SQ Sequence 9 AA;

Query Match 43.5%; Score 30; DB 22; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.4e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNDQVLEI 12
:||||:|
Db 2 mndqlmfl 9

RESULT 15
AAU06400
ID AAU06400 standard; Peptide; 9 AA.
XX
AC AAU06400;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human prostate antigen binding peptide #22.
XX
KW Prostate cancer-associated antigen; supermotif; human leukocyte antigen;
KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;
KW immunogenicity; immunosuppression; HTL.
XX
OS Homo sapiens.
XX
PN WO200145728-A2.
XX

PD 28-JUN-2001.
 XX
 PF 20-DEC-2000; 2000WO-US35516.
 XX
 PR 21-DEC-1999; 99US-0171312.
 PR 07-AUG-2000; 2000US-0633364.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;
 XX
 DR WPI; 2001-398311/42.
 XX
 PT Tumour antigen-associated group-based vaccines useful for vaccinating
 PT against prostate cancer -
 PS
 PS Example 2; Page 237; 252pp; English.
 XX
 CC The sequences represent prostate cancer-associated antigens and derived
 CC motif or supermotif epitopes. The peptide epitopes are included in
 CC prostate cancer vaccine compositions due to their ability to bind to
 CC human leukocyte antigen (HLA) molecules, which recognise the motifs.
 CC Peptides with a high binding affinity are further tested for their
 CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte
 CC (HTL) response. Supermotif-bearing peptides may also be tested for their
 CC binding affinity to multiple alleles within the HLA superfamily. The
 CC vaccine compositions can be modified, for example, to enhance
 CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to
 CC alter the immune response to suit the target disease. These group-based
 CC vaccines allow the focus of an immune response to multiple selected
 CC antigens from the same pathogen. Variability among the immune responses
 CC of patients can therefore be alleviated by the inclusion of groups from
 CC multiple antigens in a vaccine.
 XX
 SQ Sequence 9 AA:

Query Match 43.5%; Score 30; DB 22; Length 9;
 Best local Similarity 50.0%; Pred. No. 6.4e+05;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LNDQVLEI 12
 :|||::|:
 Db 2 mndqimtl 9

Search completed: June 21, 2002, 09:53:01
 Job time: 123 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:51:43 ; Search time 14.14 Seconds

(without alignments)
95.138 Million cell updates/sec

Title: US-09-780-035-33

Perfect score: 69

Sequence: 1 VIRLNDOVLFIDQ 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 2092

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	34.8	9	2	D24180
2	21.5	31.2	10	2	F44644
3	21	30.4	13	2	G44644
4	20	29.0	13	2	S08575
5	19	27.5	9	2	PT0272
6	19	27.5	11	2	S23373
7	19	27.5	12	2	S11298
8	19	27.5	14	2	PH1767
9	18	26.1	6	2	I46126
10	18	26.1	9	2	B28495
11	18	26.1	9	2	C24180
12	18	26.1	14	2	E33098
13	18	26.1	14	2	PH1763
14	17	24.6	9	2	A61386
15	17	24.6	10	2	S13224
16	17	24.6	10	2	PC044
17	17	24.6	10	2	PH0807
18	17	24.6	10	2	PH0807
19	17	24.6	12	2	S11286
20	17	24.6	12	2	E58502
21	17	24.6	12	2	PH1466
22	17	24.6	12	2	B56049
23	17	24.6	12	2	D85517
24	17	24.6	14	2	A44920
25	17	24.6	14	2	A54370
26	16	23.2	8	2	I57532
27	16	23.2	9	2	B57444
28	16	23.2	10	2	A13687
29	16	23.2	10	2	G60527

30	16	23.2	10	2	G60589	sperm-activating p
31	16	23.2	10	2	S70722	65.4k GRP-binding
32	16	23.2	10	2	B39308	glycine reductase
33	16	23.2	11	2	J02307	hypothetical 1.5k
34	16	23.2	11	2	S71304	amine oxidase (cop
35	16	23.2	11	2	A61575	trimeresurus serin
36	16	23.2	12	2	A29169	phospholipase A2 (
37	16	23.2	12	2	S71034	potB protein - Sal
38	16	23.2	12	2	S49547	hypothetical prote
39	16	23.2	12	2	PH1171	T-cell receptor al
40	16	23.2	13	2	PS0325	tetrahydroberberin
41	16	23.2	13	2	E60396	antigen 7H8/2 - ma
42	16	23.2	14	2	A39239	actin 8 - slime mo
43	16	23.2	14	2	A28018	very late antigen-
44	16	23.2	14	2	PH1614	Ig H chain V-D-J r
45	15	21.7	7	2	S29735	polysphosphate--glu

ALIGNMENTS

RESULT 1
D24180
fibrinogen beta chain - red guenon (fragment)
N:Contains: fibrinopeptide B
C:Species: Erythrocytes patas (red guenon, hussar)
C:Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C:Accession: D24180
R:Nakamura, S.; Takenaka, O.; Takahashi, X.
J. Biochem. 97, 1487-1492, 1985
A:Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey
unions, and baboons.
A:Reference number: A91990; MUID:85289140
A:Accession: D24180
A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disc

Query Match 34.8%; Score 24; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 NDQVLF 11

DB 1 NEVLE 6

RESULT 2
F44644

neurotoxin-associated protein type B Hn+ 35K chain, band 3a - Clostridium botulinum (C:Species: Clostridium botulinum
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
R:Somers, E.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A:Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without
A:Reference number: A44644; MUID:92143938
A:Accession: type B
A:Contents: type B
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:83787)
C:Keywords: hemagglutinin

Query Match 31.2%; Score 21.5; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.2e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 1; Gaps 1;
QY 2 IRN-LNDQVL 10
|:| |:::

Db 1 IONIINDKIV 10

RESULT 3

G44644

C:Species: Clostridium botulinum

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C:Accession: G44644

R:Somers, E.; Dasgupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A:Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without he

A:Reference number: A44644; MUID:92143938

A:Contents: type B

A:Accession: G44644

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <SOM>

A:Note: sequence extracted from NCBI backbone (NCBIP:83785)

C:Keywords: hemagglutinin

Query Match 30.4%; Score 21; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 1.2e+03;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNDQVL 10

Db 8 LNDKIV 13

RESULT 4

S08575

botulinum neurotoxin type E - Clostridium botulinum (strain Alaska E-43) (fragment)

C:Species: Clostridium botulinum

A:Variety: strain Alaska E-43

C>Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C:Accession: S08575

R:Schmidt, J.J.; Sathymoorthy, V.; Dasgupta, B.R.

Arch. Biochem. Biophys. 238, 544-548, 1985

A:Title: Partial amino acid sequences of botulinum neurotoxins types B and E.

A:Reference number: S07128; MUID:85197963

A:Accession: S08575

A:Molecule type: protein

A:Residues: 1-13 <SCH>

A:Experimental source: strain Alaska E-43

F:1-13/product: botulinum neurotoxin E light chain (fragment) #status predicted <LIG>

Query Match 29.0%; Score 20; DB 2; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.8e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NINDQV 9

Db 7 NYNDXV 12

RESULT 5

PT0272

Ig heavy chain CDR3 region (clone 3-103B) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0272

R:Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108357

A:Accession: PT0272

A:Molecule type: DNA

A:Residues: 1-9 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotrimer; immunoglobulin

Query Match 27.5%; Score 19; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 NINDQV 9

Db 2 NMNDEN 7

RESULT 6

S23373

T-cell receptor alpha chain J region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C:Accession: S23373

R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Elch

Eur. J. Immunol. 21, 2749-2754, 1991

A:Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of r

A:Reference number: S23364; MUID:92037820

A:Accession: S23373

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-11 <PLD>

A:Cross-references: EMBL:X58168

C:Keywords: T-cell receptor

Query Match 27.5%; Score 19; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 2.3e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 DOYLF 11

Db 7 DKVIF 11

RESULT 7

S11298

hemagglutinin precursor - influenza A virus (strain A/FPV/Rostock/34 [H7N1]) (fragment)

C:Species: influenza A virus

C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994

C:Accession: S11298

R:Robertson, J.S.

Nucleic Acids Res. 6, 3745-3757, 1979

A:Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influe

A:Reference number: S11286; MUID:80034428

A:Accession: S11298

A:Molecule type: genomic RNA

A:Residues: 1-12 <ROB>

A:Cross-references: GB:J02111

C:Genetics:

A:Map position: segment 4

C:Superfamily: influenza virus hemagglutinin

C:Keywords: homotrimer

Query Match 27.5%; Score 19; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 2.5e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 LNDQVL 10

Db 1 NNTQIL 6

RESULT 8

PH1767

T cell receptor alpha chain V region (clone 2V alpha 7.2-2) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1767

DT	01-NOV-1988 (Rel. 09, created)
DT	01-NOV-1988 (Rel. 09, last sequence update)

DT 01-NOV-1995 (Rel. 32, last annotation update)
 DE Arg-conopressin S.
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conidae; Conus.
 OX NCB1_TaxID=6493;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=8058932; PubMed=3680228;
 RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
 RA Gray W.R., Olivera B.M.;
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
 RT peptides from Conus geographus and Conus striatus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]
 RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails."
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: B28495; B28495;
 DR InterPro: IPR000981; Neurohypophys_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 26.1%; Score 18; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VIRN 4
 Db 2 IIRN 5
 RESULT 3
 ID FIBB_MAFU STANDARD; PRT; 9 AA.
 AC P19345;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, last sequence update)
 DT 01-MAR-2002 (Rel. 41, last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN FGB.
 OS Macaca fuscata fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCB1_TaxID=9543;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85289140; PubMed=3928610;
 RA Nakamura S., Takenaka O., Takahashi K.;
 RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
 RT pata monkey (Erythrocebus pata): their amino acid sequences,
 RT restricted mutations, and a molecular phylogeny for macaques,
 RT guenons, and baboons."
 RL J. Biochem. 97:1487-1492(1985).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR PIR: C24180; C24180.

DR InterPro: IPR002181; Fibrinogen_C.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN, PARTIAL.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;

Query Match 26.1%; Score 18; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 NDQVLF 11
 Db 1 NEESLF 6

RESULT 4
 ID TEME_RANTE STANDARD; PRT; 13 AA.
 AC P56920;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Temporin E.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCB1_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RP TISSUE-Skin;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Mele R., Mangoni M.L.,
 RA Barra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 RT temporaria."
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
 CC BACTERIA.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE BREVITIN/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 CC Amphibian skin; Antibiotic; Amidation; Multigene family.
 KW MOD RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match 26.1%; Score 18; DB 1; Length 13;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VIRNNDQVLF 10
 Db 4 IIGNLNSLF 13

RESULT 5
 ID HS70_PINPS STANDARD; PRT; 11 AA.
 AC P81672;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE Heat shock 70 kDa protein (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCB1_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RP TISSUE-Needle;
 RX MEDLINE=99274088; PubMed=10344291;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:52:28 ; Search time 23.84 Seconds
(without alignments)
101.591 Million cell updates/sec

Title: US-09-780-035-33
Perfect score: 69
Sequence: 1 VIRINDOVLFTDQ 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 2454

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.rodent:*
13: sp.virus:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	36.2	13	2	09R862
2	24.5	35.5	10	2	09R5N4
3	24	34.8	13	8	0957T7
4	23	33.3	9	2	048686
5	22	31.9	9	4	014715
6	22	31.9	12	2	09R5R8
7	21.5	31.2	10	2	09R5M6
8	21	30.4	8	2	09R5Z9
9	21	30.4	13	2	09R5N5
10	21	30.4	13	2	09R5Z1
11	20	29.0	14	4	096050
12	20	29.0	10	15	064980
13	20	29.0	13	2	048357
14	20	29.0	13	2	050117
15	19	27.5	9	2	09R9C4
16	19	27.5	9	12	09PYK1

17	19	27.5	9	12	09IBM8	09IBM8 simian viru
18	19	27.5	12	4	09NTR7	09NTR7 homo sapien
19	19	27.5	13	2	09R3R3	09R3R3 borrelia bu
20	19	27.5	14	2	09R457	09R457 clostridium
21	19	27.5	14	2	09R457	09R457 bacillus su
22	19	27.5	14	2	09LCS1	09LCS1 bacillus su
23	19	27.5	14	12	094072	094072 influenza a
24	19	27.5	10	4	09P158	09P158 choristoneu
25	18	26.1	11	4	09UDE8	09UDE8 homo sapien
26	18	26.1	11	10	09R4B1	09R4B1 streptococ
27	18	26.1	11	10	09AIR5	09AIR5 pinus radia
28	18	26.1	12	8	09RTU3	09RTU3 bos taurus
29	18	26.1	14	3	090342	090342 saccharomyc
30	17	25.4	13	2	031296	031296 borrelia af
31	17	24.6	8	2	P72279	P72279 rhodococcus
32	17	24.6	11	4	09T2W0	09T2W0 saccharomyc
33	17	24.6	12	6	09UCP2	09UCP2 homo sapien
34	17	24.6	12	6	09TOW3	09TOW3 bos taurus
35	17	24.6	12	10	0945C3	0945C3 cryptosporid
36	17	24.6	12	12	084038	084038 influenza a
37	17	24.6	13	2	09R7D6	09R7D6 clostridium
38	17	24.6	13	6	031295	031295 buchiera ap
39	17	24.6	13	11	09TUV6	09TUV6 ovis aries
40	17	24.6	13	11	09CS47	09CS47 mus musculu
41	17	24.6	14	2	09R506	09R506 burkholderi
42	17	24.6	14	2	060199	060199 escherichia
43	17	24.6	14	11	09QVW9	09QVW9 rattus sp.
44	16.5	23.9	11	2	073591	073591 gallus gall
45	16	23.2	8	2	09AIR7	09AIR7 candidatus
					093SR0	093SR0 staphylococ

ALIGNMENTS

RESULT 1	09R862	PRELIMINARY:	PRT:	13 AA.
AC	09R862	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-MAY-2000	(TREMBLrel. 16, Last annotation update)		
DE	2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12) (FRAGMENT).			
LEU4.				
OS	Buchnera aphidicola.			
OC	Plasmid pBSg1.			
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.			
OX	NCBI_TaxID=9;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99028904; PubMed=9812361;			
RA	Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;			
RT	"Structure and evolution of the leucine plasmids carried by the			
RT	endosymbiont (Buchnera aphidicola) from aphids of the family			
RT	Aphididae."			
RL	FEMS Microbiol. Lett. 168:43-49(1998).			
DR	EMBL: AJ006876; CAA07296.1; -			
KW	Lyase; Plasmid.			
FT	NON_TER			
FT	SEQUENCE 13 AA; 1538 MW; 1BCD22320390C050 CRC64;			

Query Match: 36.2% Score 25; DB 2; Length 13;
Best Local Similarity 44.4% Pred. No. 7.5e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 LNDQVLFID 13
Db 1 MNSQVILFD 9
RESULT 2
09R5N4 PRELIMINARY; PRT; 10 AA.

AC Q9R5N4: 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE NEUROTOXIN TYPE A HN+ 35 KDA SUBUNIT.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 CC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92143938; PubMed=1781887;
 RA Somers E., Dasgupta B.R.;
 RT "Clostridium botulinum types A, B, C1, and E produce proteins with or
 without hemagglutinating activity: do they share common amino acid
 RT sequences and genes?";
 RL J. Protein Chem. 10:415-425(1991).
 SQ SEQUENCE 10 AA; 1143 MW; CF3CB4A44735B456 CRC64;

Query Match 35.5%; Score 24.5; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 7e+02; 0; Indels 1; Gaps 1;
 Matches 6; Conservative 3; Mismatches 0;

OY 1 VIRN-LNDQV 9
 Db 1 VIONSLNDKI 10

RESULT 3
 ID 0957T7 PRELIMINARY; PRT; 13 AA.
 AC 0957T7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 OS Trichopsis pumila (Pygmy gourami).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 OC Anabantoidae; Belontiidae; Trichopsids.
 OX NCBI_TaxID=158454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang T.Y., Tzeng C.S., Shen S.C.;
 RT "Conservation and Phylogeography of Taiwan Paradise Fish, Macropodus
 RT opercularis Linnaeus.";
 RL Acta Zool. Taiwanica 10:121-134(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wang T.Y., Tzeng C.S., Shen S.C.;
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF359378; AAK51458.1;
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1443 MW; 55430C67982AAB17 CRC64;

Query Match 34.8%; Score 24; DB 8; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.1e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 LNDQVLF 11
 Db 6 LEDKILF 12

RESULT 4
 ID 048686 PRELIMINARY; PRT; 9 AA.
 AC 048686;

DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE STREPTOCOCCUS CREMORIS PROMOTER 23 DNA (FRAGMENT).
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 CC Lactococcus.
 OX NCBI_TaxID=1359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88105390; PubMed=2447829;
 RA van der Vossen J.M., van der Leije D., Venema G.;
 RT "Isolation and characterization of Streptococcus cremoris Wg2-specific
 RT promoters.";
 RL Appl. Environ. Microbiol. 53:2452-2457(1987).
 DR EMBL; M24763; AAA74720.1;
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1080 MW; 5AF3AA4AA4469443 CRC64;

Query Match 33.3%; Score 23; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 IRNLND 7
 Db 1 MKNMND 6

RESULT 5
 ID 014715 PRELIMINARY; PRT; 9 AA.
 AC 014715;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE KERATIN 14 (FRAGMENT).
 GN KRT14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Coulombe P., Hutton M., Letai A., Hebert A., Paller A., Fuchs E.;
 RT "Point mutations in human keratin 14 genes of epidermolysis bullosa
 RT simplex patients: genetic and functional analyses.";
 RL Cell 66:1301-1311(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95072587; PubMed=7526926;
 RA Yamanishi K., Matsuki M., Konishi K., Yasuno H.;
 RT "A novel mutation of keratin 12 to Phe at a highly conserved hydrophobic
 RT residue in the helix initiation motif of keratin 14 in epidermolysis
 RT bullosa simplex.";
 RL Hum. Mol. Genet. 3:1171-1172(1994).
 DR EMBL; D28807; BAA05967.1;
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 1138 MW; BE300AA449C456D6 CRC64;

Query Match 31.9%; Score 22; DB 4; Length 9;
 Best Local Similarity 37.5%; Pred. No. 5.6e+05;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 IRNLNDQV 9
 Db 2 MONENDRL 9

RESULT 6
 ID 09R5R8

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:51:18 ; Search time 12.84 Seconds

(without alignments)
26,632 Million cell updates/sec

Title: US-09-780-035-33

Perfect score: 1 VTRNNDQVLEFDQ 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 94722

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCUTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39.1	14	4	US-09-385-442-31	Sequence 31, Appl
2	36.2	10	2	US-08-764-640-67	Sequence 67, Appl
3	36.2	10	3	US-08-973-225-67	Sequence 67, Appl
4	36.2	10	3	US-09-244-298A-67	Sequence 67, Appl
5	36.2	10	4	US-09-516-704-67	Sequence 67, Appl
6	34.8	10	1	US-07-657-769B-8	Sequence 8, Appl
7	34.8	10	1	US-07-657-769B-48	Sequence 48, Appl
8	34.8	10	1	US-07-789-184-4	Sequence 4, Appl
9	34.8	10	1	US-07-789-184-10	Sequence 10, Appl
10	34.8	10	1	US-07-789-184-112	Sequence 112, Appl
11	34.8	10	1	US-07-789-184-138	Sequence 138, Appl
12	34.8	10	1	US-07-789-184-191	Sequence 191, Appl
13	34.8	10	1	US-07-789-184-191	Sequence 191, Appl
14	34.8	10	1	US-08-475-263-4	Sequence 4, Appl
15	34.8	10	1	US-08-475-263-10	Sequence 10, Appl
16	34.8	10	1	US-08-475-263-29	Sequence 29, Appl
17	34.8	10	1	US-08-475-263-112	Sequence 112, Appl
18	34.8	10	1	US-08-475-263-138	Sequence 138, Appl
19	34.8	10	1	US-08-475-263-191	Sequence 191, Appl
20	34.8	10	1	US-08-485-886-4	Sequence 4, Appl
21	34.8	10	1	US-08-485-886-10	Sequence 10, Appl
22	34.8	10	1	US-08-485-886-29	Sequence 29, Appl
23	34.8	10	1	US-08-485-886-112	Sequence 112, Appl
24	34.8	10	1	US-08-485-886-138	Sequence 138, Appl
25	34.8	10	1	US-08-485-886-191	Sequence 191, Appl
26	34.8	10	2	US-08-477-362-4	Sequence 4, Appl
27	34.8	10	2	US-08-477-362-10	Sequence 10, Appl

28	34.8	10	2	US-08-477-362-29	Sequence 29, Appl
29	34.8	10	2	US-08-477-362-112	Sequence 112, Appl
30	34.8	10	2	US-08-477-362-138	Sequence 138, Appl
31	34.8	10	2	US-08-477-362-191	Sequence 191, Appl
32	34.8	10	2	US-08-477-134-4	Sequence 4, Appl
33	34.8	10	2	US-08-477-134-10	Sequence 10, Appl
34	34.8	10	2	US-08-477-134-29	Sequence 29, Appl
35	34.8	10	2	US-08-477-134-112	Sequence 112, Appl
36	34.8	10	2	US-08-477-134-138	Sequence 138, Appl
37	34.8	10	2	US-08-477-134-191	Sequence 191, Appl
38	34.8	10	2	US-08-483-506A-11	Sequence 11, Appl
39	34.8	10	3	US-08-473-489A-4	Sequence 4, Appl
40	34.8	10	3	US-08-473-489A-10	Sequence 10, Appl
41	34.8	10	3	US-08-473-489A-29	Sequence 29, Appl
42	34.8	10	3	US-08-473-489A-112	Sequence 112, Appl
43	34.8	10	3	US-08-473-489A-138	Sequence 138, Appl
44	34.8	10	3	US-08-473-489A-191	Sequence 191, Appl
45	34.8	10	3	US-08-485-695-4	Sequence 4, Appl

ALIGNMENTS

```

RESULT 1
US-09-385-442-31
; Sequence 31, Application US/09385442
; Patent No. 6200954
; GENERAL INFORMATION:
; APPLICANT: Ge, Ruwen
; APPLICANT: Kini, R. Manjunatha
; TITLE OF INVENTION: Small Peptides Having Potent Anti-Angiogenic Activity
; FILE REFERENCE: 1781-170P
; CURRENT APPLICATION NUMBER: US/09/385,442
; EARLIER FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 60/099,313
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PR
; ORGANISM: mammalian
; FEATURE:
; OTHER INFORMATION: Endo-3
US-09-385-442-31

Query Match          39.1% Score 27; DB 4; Length 14;
Best Local Similarity 66.7%; Pred. NO. 63;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRLNDQVL 10
Db 3 IRLNDQVL 11

RESULT 2
US-08-764-640-67
; Sequence 67, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Bairett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagsstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Depirine, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun

```

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-764-640-67

Query Match 36.2%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NINDOYLE 11
DB 2 NRNDLLLF 9

RESULT 3
US-08-973-225-67
Sequence 67, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haseiden, Sherill S.
Matheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-08-973-225-67

Query Match 36.2%; Score 25; DB 3; Length 10;
Best Local Similarity 62.5%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NINDOYLE 11
DB 2 NRNDLLLF 9

RESULT 4
US-09-244-298A-67
Sequence 67, Application US/09244298A
Patent No. 6121238
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palanlappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Poddaturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:40 ; Search time 109.39 Seconds

(without alignments)
94.868 Million cell updates/sec

Title: US-09-780-035-28

Perfect score: 572

Sequence: 1 LVQPGSLRLSCAASGFTFS.....DDDDYDFDYGRGIMVYSS 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : PIR.71.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	522.5	91.3	119	2 S31107	Ig heavy chain - h
2	522	91.3	112	2 PH1647	Ig heavy chain - h
3	515.5	90.1	140	2 S31588	Ig heavy chain - h
4	513.5	89.8	119	2 C36005	Ig heavy chain - h
5	511.5	89.4	119	2 S31108	Ig heavy chain - h
6	510.5	89.2	119	2 D36005	Ig heavy chain - h
7	508.5	88.9	138	2 S31666	Ig heavy chain - h
8	507	88.6	120	2 S48798	Ig heavy chain - h
9	506.5	88.5	123	2 S31114	Ig heavy chain - h
10	506.5	88.5	127	2 S38489	Ig heavy chain - h
11	505.5	88.4	109	2 PH1649	Ig heavy chain - h
12	504	88.1	108	2 PH1648	Ig heavy chain - h
13	503.5	88.0	140	2 S31686	Ig heavy chain - h
14	496.5	86.8	134	2 S31699	Ig heavy chain - h
15	494.5	86.5	121	2 I53673	Ig heavy chain - h
16	488.5	85.4	160	2 S05271	Ig heavy chain - h
17	487	85.1	124	2 S20782	Ig heavy chain - h
18	482	84.3	120	2 S44111	Ig heavy chain - h
19	478.5	83.7	121	2 S31113	Ig heavy chain - h
20	477	83.4	110	2 PH1652	Ig heavy chain - h
21	475.5	83.1	121	2 G36005	Ig heavy chain - h
22	470.5	82.3	109	2 PH1646	Ig heavy chain - h
23	469	82.0	128	2 S26790	Ig heavy chain - h
24	468.5	81.9	125	2 S30531	Ig heavy chain - h
25	466.5	81.6	119	2 F36005	Ig heavy chain - h
26	464.5	81.2	140	2 A30532	Ig heavy chain - h
27	463	80.9	120	2 S36278	Ig heavy chain - h
28	463	80.9	118	2 S31105	Ig heavy chain - h
29	462.5	80.9	111	2 PH1645	Ig heavy chain - h

30	462	80.8	114	2 S46391	Ig heavy chain - h
31	461	80.6	114	2 S31120	Ig heavy chain - h
32	461	80.6	118	2 S31116	Ig heavy chain - h
33	460	80.4	114	2 S46390	Ig heavy chain - h
34	460	80.4	120	2 E46590	Ig heavy chain - h
35	459	80.2	147	2 I37780	Ig heavy chain - h
36	458.5	80.2	123	2 S26794	Ig heavy chain - h
37	458.5	80.2	132	2 S31603	Ig heavy chain - h
38	458.5	80.2	134	2 S31679	Ig heavy chain - h
39	458	80.1	140	2 S70442	Ig heavy chain - h
40	457	79.9	122	2 E36005	Ig heavy chain - h
41	457	79.9	141	2 S31669	Ig heavy chain - h
42	454.5	79.5	109	2 PH1644	Ig heavy chain - h
43	454.5	79.5	135	2 S31598	Ig heavy chain - h
44	454	79.4	98	2 S26889	Ig heavy chain - h
45	454	79.4	114	2 S46392	Ig heavy chain - h

ALIGNMENTS

RESULT 1
S31107
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur, Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633
A:Accession: S31107
A:Molecule type: mRNA
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62955
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 91.3%; Score 522.5; DB 2; Length 119;
Best Local Similarity 92.7%; Pred No. 5.3e-41;
Matches 101; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
QY 1 LVQPGSLRLSCAASGFTFSYAMSWRQAPGKLEWVAISGSGSTYADSVKGRFTI 60
DB 11 LVQPGSLRLSCAASGFTFSYAMSWRQAPGKLEWVAISGSGSTYADSVKGRFTI 70
QY 61 SRDKNITLYLQMSLRADTAIVYTCARDD-DYDFDYGRGIMVYSS 108
DB 71 SRDKNITLYLQMSLRADTAIVYTCARDD-DYDFDYGRGIMVYSS 119
RESULT 2
PH1647
Ig heavy chain V region (clone 2D10) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1647
J: Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staph
A:Reference number: PH1642; MUID:93301610
A:Accession: PH1647
A:Molecule type: mRNA
A:Residues: 1-112 <HIL>
A:Experimental source: B cell
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 91.3%; Score 522; DB 2; Length 112;
 Best Local Similarity 92.7%; Pred. No. 5.5e-41;
 Matches 102; Conservative 4; Mismatches 2; Indels 2; Gaps 2;

QY 1 LVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 60
 :|||||
 DB 3 VVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 62

QY 61 SRDNSKNTLYLQMSLRAEDTAVYICAKRDYDFDYGSGTLYTVSS 108
 :|||||
 DB 63 SRDNSKNTLYLQMSLRAEDTAVYICAKRDYDFDYGSGTLYTVSS 112

RESULT 3
 331588
 Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31588
 R/Cuissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31588
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-140 <CUI>
 A/Cross-references: EMBL:Z14200; NID:930957; PIDN:CAA78569.1; PID:930958
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.1%; Score 515.5; DB 2; Length 140;
 Best Local Similarity 90.1%; Pred. No. 2.7e-40;
 Matches 100; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

QY 1 LVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 60
 :|||||
 DB 30 LVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 89

QY 61 SRDNSKNTLYLQMSLRAEDTAVYICARDDDD--FDYWGSGTMYTVSS 108
 :|||||
 DB 90 SRDNSKNTLYLQMSLRAEDTAVYICAKHDYSNYIFDYWGSGTLYTVSS 140

RESULT 4
 336005
 Ig heavy chain V region (30p1) - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
 C/Accession: C36005
 R/Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A/Reference number: A36005; MUID:90349571
 A/Accession: C36005
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-119 <SCH>
 A/Cross-references: GB:M18513
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 513.5; DB 2; Length 119;
 Best Local Similarity 91.7%; Pred. No. 3.5e-40;
 Matches 100; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 LVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 60
 :|||||

DB 11 LVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 70
 QY 61 SRDNSKNTLYLQMSLRAEDTAVYICARDD--DYDFDYGSGTMYTVSS 108
 :|||||
 DB 71 SRDNSKNTLYLQMSLRAEDTAVYICADACGSGFDYWGSGTLYTVSS 119

RESULT 5
 331108
 Ig heavy chain - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C/Accession: S31108
 R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
 Eur. J. Immunol. 22, 247-251, 1992
 A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
 A/Reference number: S31104; MUID:92111633
 A/Accession: S31108
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-119 <RAA>
 A/Cross-references: EMBL:X62956
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 511.5; DB 2; Length 119;
 Best Local Similarity 91.7%; Pred. No. 5.4e-40;
 Matches 100; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 LVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 60
 :|||||
 DB 11 LVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 70

QY 61 SRDNSKNTLYLQMSLRAEDTAVYICARDD--DYDFDYGSGTMYTVSS 108
 :|||||
 DB 71 SRDNSKNTLYLQMSLRAEDTAVYICARDDRLTGTFDYGSGTLYTVSS 119

RESULT 6
 D36005
 Ig heavy chain V region (M43) - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
 C/Accession: D36005
 R/Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable ge
 A/Reference number: A36005; MUID:90349571
 A/Accession: D36005
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-119 <SCH>
 A/Cross-references: GB:M34024
 C/Genetics:
 A/Gene: IGH@; IGHDX1
 A/Cross-references: GDB:118731; OMIM:146910
 A/Map position: 14q32.33-14q32.33
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.2%; Score 510.5; DB 2; Length 119;
 Best Local Similarity 91.7%; Pred. No. 6.6e-40;
 Matches 100; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 LVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 60
 :|||||
 DB 11 LVOPGSLRLSCAAGTFFSSYAMSWVRQAPGKLEWNSAISGGSGSTYYADSVKGRFTI 70

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:48:14 ; Search time 52.75 Seconds
(without alignments)
79.274 Million cell updates/sec

Title: US-09-780-035-28

Perfect score: 572
Sequence: 1 LVQPGSURLSCAASGFTFS.....DDDDYDPDYGRTMTVSS 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450	78.7	117	1	HV3C_HUMAN
2	443	77.4	122	1	HV3G_HUMAN
3	440.5	77.0	121	1	HV3J_HUMAN
4	420.5	73.5	115	1	HV3D_HUMAN
5	414	72.4	114	1	HV3B_HUMAN
6	411	71.9	122	1	HV3A_HUMAN
7	409	71.5	122	1	HV3H_HUMAN
8	408	71.3	136	1	HV16_MOUSE
9	407	71.2	126	1	HV3K_HUMAN
10	405.5	70.9	115	1	HV3F_HUMAN
11	402.5	70.4	116	1	HV05_CARAU
12	402.5	70.4	119	1	HV3I_HUMAN
13	398.5	69.7	117	1	HV02_CANFA
14	397.5	69.5	120	1	HV3E_HUMAN
15	392	68.5	116	1	HV3T_HUMAN
16	392	68.5	119	1	HV3M_HUMAN
17	392	68.5	119	1	HV3N_HUMAN
18	384	67.1	111	1	HV35_MOUSE
19	384	67.1	114	1	HV01_CANFA
20	381	66.6	117	1	HV04_MOUSE
21	381	66.6	120	1	HV3U_HUMAN
22	379.5	66.3	97	1	HV56_MOUSE
23	377.5	66.0	123	1	HV22_MOUSE
24	376.5	65.8	115	1	HV32_MOUSE
25	376.5	65.8	123	1	HV25_MOUSE
26	375	65.6	117	1	HV55_MOUSE
27	374.5	65.5	113	1	HV30_MOUSE
28	371.5	64.9	119	1	HV3L_HUMAN
29	371.5	64.9	123	1	HV19_MOUSE
30	371	64.9	119	1	HV38_MOUSE
31	370	64.7	112	1	HV20_MOUSE
32	369.5	64.6	113	1	HV27_MOUSE
33	369.5	64.6	142	1	HV01_RAT

34	368	64.3	119	1	HV40_MOUSE	P01810 mus musculu
35	367.5	64.2	117	1	HV17_MOUSE	P01786 mus musculu
36	367.5	64.2	123	1	HV18_MOUSE	P01787 mus musculu
37	365.5	63.9	113	1	HV31_MOUSE	P01800 mus musculu
38	365.5	63.9	115	1	HV33_MOUSE	P01802 mus musculu
39	365	63.8	119	1	HV37_MOUSE	P01807 mus musculu
40	364	63.6	117	1	HV30_HUMAN	P01776 mus musculu
41	363.5	63.5	113	1	HV28_MOUSE	P01797 mus musculu
42	363.5	63.5	117	1	HV41_MOUSE	P01811 mus musculu
43	363	63.5	122	1	HV21_MOUSE	P01790 mus musculu
44	362.5	63.4	123	1	HV23_MOUSE	P01792 mus musculu
45	361.5	63.2	144	1	HV26_MOUSE	P01795 mus musculu

ALIGNMENTS

RESULT	ID	Sequence	Score	Length	DB ID	Description
1	HV3C_HUMAN	105224	450	117	1	HV3C_HUMAN
2	HV3G_HUMAN	105224	443	122	1	HV3G_HUMAN
3	HV3J_HUMAN	105224	440.5	121	1	HV3J_HUMAN
4	HV3D_HUMAN	105224	420.5	115	1	HV3D_HUMAN
5	HV3B_HUMAN	105224	414	114	1	HV3B_HUMAN
6	HV3A_HUMAN	105224	411	122	1	HV3A_HUMAN
7	HV3H_HUMAN	105224	409	122	1	HV3H_HUMAN
8	HV16_MOUSE	105224	408	136	1	HV16_MOUSE
9	HV3K_HUMAN	105224	407	126	1	HV3K_HUMAN
10	HV3F_HUMAN	105224	405.5	115	1	HV3F_HUMAN
11	HV05_CARAU	105224	402.5	116	1	HV05_CARAU
12	HV3I_HUMAN	105224	402.5	119	1	HV3I_HUMAN
13	HV02_CANFA	105224	398.5	117	1	HV02_CANFA
14	HV3E_HUMAN	105224	397.5	120	1	HV3E_HUMAN
15	HV3T_HUMAN	105224	392	116	1	HV3T_HUMAN
16	HV3M_HUMAN	105224	392	119	1	HV3M_HUMAN
17	HV3N_HUMAN	105224	392	119	1	HV3N_HUMAN
18	HV35_MOUSE	105224	384	111	1	HV35_MOUSE
19	HV01_CANFA	105224	384	114	1	HV01_CANFA
20	HV04_MOUSE	105224	381	117	1	HV04_MOUSE
21	HV3U_HUMAN	105224	381	120	1	HV3U_HUMAN
22	HV56_MOUSE	105224	379.5	97	1	HV56_MOUSE
23	HV22_MOUSE	105224	377.5	123	1	HV22_MOUSE
24	HV32_MOUSE	105224	376.5	115	1	HV32_MOUSE
25	HV25_MOUSE	105224	376.5	123	1	HV25_MOUSE
26	HV55_MOUSE	105224	375	117	1	HV55_MOUSE
27	HV30_MOUSE	105224	374.5	113	1	HV30_MOUSE
28	HV3L_HUMAN	105224	371.5	119	1	HV3L_HUMAN
29	HV19_MOUSE	105224	371.5	123	1	HV19_MOUSE
30	HV38_MOUSE	105224	371	119	1	HV38_MOUSE
31	HV20_MOUSE	105224	370	112	1	HV20_MOUSE
32	HV27_MOUSE	105224	369.5	113	1	HV27_MOUSE
33	HV01_RAT	105224	369.5	142	1	HV01_RAT

RESULT	ID	Sequence	Score	Length	DB ID	Description
1	HV3C_HUMAN	105224	450	117	1	HV3C_HUMAN
2	HV3G_HUMAN	105224	443	122	1	HV3G_HUMAN
3	HV3J_HUMAN	105224	440.5	121	1	HV3J_HUMAN
4	HV3D_HUMAN	105224	420.5	115	1	HV3D_HUMAN
5	HV3B_HUMAN	105224	414	114	1	HV3B_HUMAN
6	HV3A_HUMAN	105224	411	122	1	HV3A_HUMAN
7	HV3H_HUMAN	105224	409	122	1	HV3H_HUMAN
8	HV16_MOUSE	105224	408	136	1	HV16_MOUSE
9	HV3K_HUMAN	105224	407	126	1	HV3K_HUMAN
10	HV3F_HUMAN	105224	405.5	115	1	HV3F_HUMAN
11	HV05_CARAU	105224	402.5	116	1	HV05_CARAU
12	HV3I_HUMAN	105224	402.5	119	1	HV3I_HUMAN
13	HV02_CANFA	105224	398.5	117	1	HV02_CANFA
14	HV3E_HUMAN	105224	397.5	120	1	HV3E_HUMAN
15	HV3T_HUMAN	105224	392	116	1	HV3T_HUMAN
16	HV3M_HUMAN	105224	392	119	1	HV3M_HUMAN
17	HV3N_HUMAN	105224	392	119	1	HV3N_HUMAN
18	HV35_MOUSE	105224	384	111	1	HV35_MOUSE
19	HV01_CANFA	105224	384	114	1	HV01_CANFA
20	HV04_MOUSE	105224	381	117	1	HV04_MOUSE
21	HV3U_HUMAN	105224	381	120	1	HV3U_HUMAN
22	HV56_MOUSE	105224	379.5	97	1	HV56_MOUSE
23	HV22_MOUSE	105224	377.5	123	1	HV22_MOUSE
24	HV32_MOUSE	105224	376.5	115	1	HV32_MOUSE
25	HV25_MOUSE	105224	376.5	123	1	HV25_MOUSE
26	HV55_MOUSE	105224	375	117	1	HV55_MOUSE
27	HV30_MOUSE	105224	374.5	113	1	HV30_MOUSE
28	HV3L_HUMAN	105224	371.5	119	1	HV3L_HUMAN
29	HV19_MOUSE	105224	371.5	123	1	HV19_MOUSE
30	HV38_MOUSE	105224	371	119	1	HV38_MOUSE
31	HV20_MOUSE	105224	370	112	1	HV20_MOUSE
32	HV27_MOUSE	105224	369.5	113	1	HV27_MOUSE
33	HV01_RAT	105224	369.5	142	1	HV01_RAT

RESULT	ID	Sequence	Score	Length	DB ID	Description
1	HV3C_HUMAN	105224	450	117	1	HV3C_HUMAN
2	HV3G_HUMAN	105224	443	122	1	HV3G_HUMAN
3	HV3J_HUMAN	105224	440.5	121	1	HV3J_HUMAN
4	HV3D_HUMAN	105224	420.5	115	1	HV3D_HUMAN
5	HV3B_HUMAN	105224	414	114	1	HV3B_HUMAN
6	HV3A_HUMAN	105224	411	122	1	HV3A_HUMAN
7	HV3H_HUMAN	105224	409	122	1	HV3H_HUMAN
8	HV16_MOUSE	105224	408	136	1	HV16_MOUSE
9	HV3K_HUMAN	105224	407	126	1	HV3K_HUMAN
10	HV3F_HUMAN	105224	405.5	115	1	HV3F_HUMAN
11	HV05_CARAU	105224	402.5	116	1	HV05_CARAU
12	HV3I_HUMAN	105224	402.5	119	1	HV3I_HUMAN
13	HV02_CANFA	105224	398.5	117	1	HV02_CANFA
14	HV3E_HUMAN	105224	397.5	120	1	HV3E_HUMAN
15	HV3T_HUMAN	105224	392	116	1	HV3T_HUMAN
16	HV3M_HUMAN	105224	392	119	1	HV3M_HUMAN
17	HV3N_HUMAN	105224	392	119	1	HV3N_HUMAN
18	HV35_MOUSE	105224	384	111	1	HV35_MOUSE
19	HV01_CANFA	105224	384	114	1	HV01_CANFA
20	HV04_MOUSE	105224	381	117	1	HV04_MOUSE
21	HV3U_HUMAN	105224	381	120	1	HV3U_HUMAN
22	HV56_MOUSE	105224	379.5	97	1	HV56_MOUSE
23	HV22_MOUSE	105224	377.5	123	1	HV22_MOUSE
24	HV32_MOUSE	105224	376.5	115	1	HV32_MOUSE
25	HV25_MOUSE	105224	376.5	123	1	HV25_MOUSE
26	HV55_MOUSE	105224	375	117	1	HV55_MOUSE
27	HV30_MOUSE	105224	374.5	113	1	HV30_MOUSE
28	HV3L_HUMAN	105224	371.5	119	1	HV3L_HUMAN
29	HV19_MOUSE	105224	371.5	123	1	HV19_MOUSE
30	HV38_MOUSE	105224	371	119	1	HV38_MOUSE
31	HV20_MOUSE	105224	370	112	1	HV20_MOUSE
32	HV27_MOUSE	105224	369.5	113	1	HV27_MOUSE
33	HV01_RAT	105224	369.5	142	1	HV01_RAT

Query Match	77.4%;	Score 443;	DB 1;	Length 122;
Best Local Similarity	75.0%;	Pred. No. 2.7e-39;		
Matches	84;	Conservative 11;	Mismatches 13;	Indels 4;
			Gaps	1

RESULT	3
HV3J_HUMAN	
ID	HV3J_HUMAN
STANDARD;	
PRT;	121 AA

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-III region HLL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
 RT "Amino acid sequence of the VH region of human myeloma
 R7 cryoglobulin IgG H1.1";
 RL Biochemistry 18:553-560(1977).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGCI MYELOMA
 CC PROTEIN.
 CC PIR: A02054; G1HUH.
 DR HSSP: P01772; 2F8A.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003536; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; Igv_1.
 KW Immunoglobulin V region.

Query Match	77.0%;	Score 440.5;	DB 1;	Length 121;
Best Local Similarity	74.8%;	Pred. No. 4.9e-39;		
Matches 83; Conservative		9;	Mismatches 16;	Indels 3; Gaps 1;

RESULT	4	
HV3D_HUMAN		
ID	HV3D_HUMAN	STANDARD;
		PRT; 115 AA.

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DN      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig heavy chain V-III region TIL.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RN      SEQUENCE.
RX      MEDLINE=78005528; PubMed=409716;
RA      Wang A.-C., Wang I.-Y., Fudenberg H.H.;
RT      "Immunoglobulin structure and genetics. Identity between variable
RT      regions of a mu and a gamma2 chain."
RL      J. Biol. Chem. 252:7192-7199(1977).
-1      MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
        OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
        GAMMAPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
        IDENTICAL.
DR      PIR: A02048; H3HUTL.
DR      InterPro: IPR003506; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
DR      Immunoglobulin V region.
KT      NON_TER      115      115
SO      SEQUENCE      115 AA; 12356 MW; 4DC6C7D179F62326 CRC64;

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Query Match	73.5%;	Score 420.5;	DB 1;	Length 115;
Best Local Similarity	76.1%;	Pred. No. 5.5e-37;		
Matches	83;	Conservative	7;	Mismatches 14; Indels 5; Gaps 2;

Qy	Db
61	11
SRDSSKLTLYLQNSLRADETAYVYICARD- DIDFDYMGAGTVYVYSS	LVPGGSLRLSCAASFFSTSTYVMWVRQAPGKGLZLGLSTLSZSYAASVYKGRFTI
108	700
71	11
SRDSSKLT-----MNSLRADETAYVYICAGKSAAYFEBWVGGLTVYSS	LVPGGSLRLSCAASFFSTSTYVMWVRQAPGKGLZLGLSTLSZSYAASVYKGRFTI
115	700

RESULT	5		
HY3B_HUMAN			
HY3B_HUMAN	STANDARD;	PRT;	114 AA.
AC	P01763		
DT	21-JUL-1986	(rel. 01, Created)	
DT	21-JUL-1986	(rel. 01, Last sequence update)	
DT	15-JUL-1999	(rel. 38, Last annotation update)	
DE	Ig heavy chain V-III region WEA. Homo sapiens (Human).		

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:16 ; Search time 194.32 Seconds

(without alignments)
96.148 Million cell updates/sec

Title: US-09-780-035-28

Sequence: 1 LVOPGSLRLSCAASGFTFS.....DDDDYDPDYWGKGTWTVSS 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	497.5	87.0	597	4 Q96BB9	Q96BB9 homo sapien
2	467.5	81.7	121	4 Q9UL71	Q9UL71 homo sapien
3	463	80.9	118	4 Q9UL91	Q9UL91 homo sapien
4	453.5	79.3	113	4 Q9UL90	Q9UL90 homo sapien
5	446	78.0	118	4 Q9UL72	Q9UL72 homo sapien
6	439.5	76.8	116	4 Q9UL93	Q9UL93 homo sapien
7	439	76.7	112	4 Q9HCC1	Q9HCC1 homo sapien
8	438	76.6	147	4 Q9Y509	Q9Y509 homo sapien
9	433.5	75.8	119	11 Q920E7	Q920E7 mus musculu
10	432	75.5	494	4 Q96K68	Q96K68 homo sapien
11	428	74.8	122	4 Q9UL84	Q9UL84 homo sapien
12	419	73.3	487	11 Q99KA4	Q99KA4 mus musculu
13	408.5	71.4	479	11 Q91WP5	Q91WP5 mus musculu
14	403	70.5	473	11 Q91Z05	Q91Z05 mus musculu
15	400.5	70.0	112	4 Q9UGP3	Q9UGP3 homo sapien
16	389	68.0	95	4 Q9ULB6	Q9ULB6 homo sapien

17	387.5	67.7	131	4 Q9UL88	Q9UL88 homo sapien
18	387.5	67.7	480	11 Q91XE1	Q91XE1 mus musculu
19	383.5	67.0	104	4 Q9UL87	Q9UL87 homo sapien
20	383.5	67.0	486	11 Q91Z07	Q91Z07 mus musculu
21	381	66.6	437	11 Q9RI44	Q9RI44 mus musculu
22	358	62.6	298	11 Q9QYF0	Q9QYF0 mus musculu
23	353	61.7	124	4 Q9UL92	Q9UL92 homo sapien
24	342.5	59.9	473	11 Q9D8L4	Q9D8L4 mus sapien
25	342	59.8	143	11 Q924R0	Q924R0 mus musculu
26	341	59.6	145	11 Q924R4	Q924R4 mus musculu
27	339	59.3	124	6 Q9N0W6	Q9N0W6 oryctolagus
28	339	59.3	124	6 Q9N0M4	Q9N0M4 oryctolagus
29	337.5	59.0	484	11 Q99LA6	Q99LA6 mus musculu
30	334.5	58.5	117	11 Q9QXF0	Q9QXF0 mus musculu
31	330	57.7	109	11 Q9JL75	Q9JL75 mus musculu
32	328.5	57.4	146	11 Q924Q3	Q924Q3 mus musculu
33	326	57.0	159	4 Q96Q50	Q96Q50 homo sapien
34	326	56.8	241	11 Q921A6	Q921A6 mus musculu
35	325	56.8	145	11 Q924P7	Q924P7 mus musculu
36	324	56.6	143	11 Q91V67	Q91V67 mus musculu
37	323	56.5	145	11 Q924R1	Q924R1 mus musculu
38	322.5	56.4	117	11 Q9QXE9	Q9QXE9 mus musculu
39	322.5	56.4	140	11 Q924P8	Q924P8 mus musculu
40	321.5	56.2	119	5 Q9GYZ2	Q9GYZ2 schistosoma
41	321	56.1	182	11 Q91X92	Q91X92 mus musculu
42	320.5	56.0	125	4 Q9UL95	Q9UL95 homo sapien
43	320	55.9	143	4 Q924Q0	Q924Q0 mus musculu
44	319	55.8	116	4 Q9UL89	Q9UL89 homo sapien
45	319	55.8	463	11 Q99LC4	Q99LC4 mus musculu

ALIGNMENTS

RESULT 1

Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.

AC Q96BB9: 01-DEC-2001 (TRENBLER, 19, Created)

DT 01-DEC-2001 (TRENBLER, 19, Last sequence update)

DT 01-DEC-2001 (TRENBLER, 19, Last annotation update)

DE HYPOTHETICAL 65.0 KDA PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PRIMARY B-CELLS FROM TONSILS;

RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC015760; AH015760.1; -.

KW Hypothetical protein.

SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 87.0%; Score 497.5; DB 4; Length 597;

Best Local Similarity 83.5%; Pred. No. 1.7e+43;

Matches 96; Conservative 7; Mismatches 5; Indels 7; Gaps 1;

QY 1 LVOPGSLRLSCAASGFTFSYAMSWYRQAPGKLEWVSAISGSGSTYADSVKGRFTI 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 30 LVOPGSLRLSCAASGFTFSYAMSWYRQAPGKLEWVSAISGSGSTYADSVKGRFTI 89

QY 61 SRDKNKTLTYLQNNLSRAEDTAVYYCARDDDDYDF-----DYWGKGTWTVSS 108

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 90 SRDKNKTLTYLQNNLSRAEDTAVYYCARDDDDYDF-----DYWGKGTWTVSS 144

RESULT 2

Q9UL71 ID Q9UL71 PRELIMINARY; PRT; 121 AA.

AC Q9UL71:

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035043; AAD56279.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1 1
FT 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFASD50736 CRC64;

Query Match 81.7%; Score 467.5; DB 4; Length 121;
Best Local Similarity 82.9%; Pred. No. 2.9e-41;
Matches 92; Conservative 5; Mismatches 11; Indels 3; Gaps 2;

QY 1 LVOPGSLRLSCAASGFTSSYAMSVWROAPGKLEWVAISGSGSTYYADSVKGRFTI 60
Db 11 VVOPGSLRLSCAASGFTSSYAMSVWROAPGKLEWVAISGSGSTYYADSVKGRFTI 70
11 VVOPGSLRLSCAASGFTSSYAMSVWROAPGKLEWVAISGSGSTYYADSVKGRFTI 70
QY 61 SRDMSKNTLYLQMSLRADTAIVYCARDDDDYDFTYGRGTWTVSS 108
Db 71 SRDMSKNTLYLQMSLRADTAIVYCARDDDDYDFTYGRGTWTVSS 121

RESULT 3
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035023; AAD56259.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1 1
FT 118 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 80.9%; Score 463; DB 4; Length 118;
Best Local Similarity 83.2%; Pred. No. 8.3e-41;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 LVOPGSLRLSCAASGFTSSYAMSVWROAPGKLEWVAISGSGSTYYADSVKGRFTI 60
Db 11 VVOPGSLRLSCAASGFTSSYAMSVWROAPGKLEWVAISGSGSTYYADSVKGRFTI 70
11 VVOPGSLRLSCAASGFTSSYAMSVWROAPGKLEWVAISGSGSTYYADSVKGRFTI 70
QY 61 SRDMSKNTLYLQMSLRADTAIVYCARDDDDYDFTYGRGTWTVSS 107
Db 71 SRDMSKNTLYLQMSLRADTAIVYCARDDDDYDFTYGRGTWTVSS 117

RESULT 4
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035024; AAD56260.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1 1
FT 113 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 79.3%; Score 453.5; DB 4; Length 113;
Best Local Similarity 80.6%; Pred. No. 7.7e-40;
Matches 87; Conservative 7; Mismatches 9; Indels 5; Gaps 1;

QY 1 LVOPGSLRLSCAASGFTSSYAMSVWROAPGKLEWVAISGSGSTYYADSVKGRFTI 60
Db 11 VVOPGSLRLSCAASGFTSSYAMSVWROAPGKLEWVAISGSGSTYYADSVKGRFTI 70
11 VVOPGSLRLSCAASGFTSSYAMSVWROAPGKLEWVAISGSGSTYYADSVKGRFTI 70
QY 61 SRDMSKNTLYLQMSLRADTAIVYCARDDDDYDFTYGRGTWTVSS 108
Db 71 SRDMSKNTLYLQMSLRADTAIVYCARDDDDYDFTYGRGTWTVSS 113

RESULT 5
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:14 ; Search time 245.49 Seconds

(without alignments)
48.865 Million cell updates/sec

Title: US-09-780-035-28

Perfect score: 572

Sequence: 1 LVPEGSGRLSCASAGFTFS.....DDDDYDPDYGRTMTVSS 108

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802:*
1: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1984.DAT:*
6: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1985.DAT:*
7: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1986.DAT:*
8: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1987.DAT:*
9: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1988.DAT:*
10: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1989.DAT:*
11: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1990.DAT:*
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13: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1992.DAT:*
14: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1993.DAT:*
15: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1994.DAT:*
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17: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1996.DAT:*
18: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	100.0	108	22	AA65318
2	572	100.0	118	22	AA65354
3	572	100.0	235	22	AA65320
4	517	90.4	120	18	AAW27553
5	517	90.4	281	18	AAW27560
6	515	90.0	128	22	AAE07014
7	515	90.0	140	18	AAW13524
8	512.5	89.6	313	22	AAU14320
9	511.5	89.4	121	22	AAE07029
10	511.5	89.4	125	22	AAE07013
11	510	89.2	124	22	AAE07026

12	509	89.0	122	20	AAW78432
13	509	88.0	240	20	AAO2472
14	508.5	88.9	240	21	AAV15124
15	508.5	88.9	240	21	AAV15125
16	506.5	88.5	113	19	AAW70621
17	506.5	88.5	113	21	AAW82347
18	506.5	88.5	115	21	AAV96064
19	506	88.5	240	22	AAW46038
20	505.5	88.4	245	22	AAW67620
21	505	88.3	120	22	AAE07022
22	503.5	88.0	119	22	AAW62088
23	503.5	88.0	119	22	AAW60401
24	503.5	88.0	119	22	AAW61586
25	503.5	88.0	123	22	AAE07019
26	503	87.9	124	18	AAW13537
27	503	87.9	131	18	AAW13520
28	502	87.8	120	22	AAU02508
29	502	87.8	293	22	AAW65715
30	500.5	87.5	119	22	AAU02512
31	500.5	87.5	159	22	AAU14226
32	499.5	87.3	127	22	AAE07024
33	499	87.2	116	22	AAE07017
34	499	87.2	240	22	AAW46040
35	496	86.7	443	18	AAW13564
36	495.5	86.6	130	19	AAW71048
37	494	86.4	122	14	AAW30773
38	493.5	86.3	246	21	AAW58235
39	493	86.2	123	22	AAW62748
40	493	86.2	240	22	AAW46052
41	492.5	86.1	117	22	AAE12061
42	492.5	86.1	119	22	AAU02525
43	492	86.0	116	18	AAW13529
44	491	85.8	128	18	AAW06242
45	490.5	85.8	130	19	AAW71047

ALIGNMENTS

RESULT	1
AA65318	
ID	AA65318 standard; protein; 108 AA.
AC	AA65318;
XX	
DT	30-NOV-2001 (first entry)
XX	
DE	Anti-IL-18 antibody LT28 heavy chain sequence.
KW	IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW	nocrotropic; neurotoxic; antineoplastic; antiparkinsonian; cardiatic;
XX	immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
XX	
OS	Homo sapiens.
XX	
PN	WO200158956-A2.
XX	
PD	16-AUG-2001.
XX	
PF	09-FEB-2001; 2001WO-US04170.
XX	
PR	10-FEB-2000; 2000US-0181608.
XX	
PA	(BADI) BASF AG.
XX	
PI	Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfield J;
PI	Duncan AR, Brocklehurst SM, Mankovich J, Shorrocks CP, Thompson JE;
PI	Lenard SN.
XX	
DR	WPI; 2001-550020/61.
XX	
DR	N-PSDB; AAH47513.
XX	
PT	Novel antibodies and compounds capable of binding to human

Antibody heavy cha
A single chain ant
Anti-human CTLA-4
Anti-murine CTLA-4
Human consensus fr
Human consensus se
Human anti-DAF ant
Human TF anti-Idio
Human leukocyte an
Human heavy chain
Human Yh consensus
Consensus human be
Human variable hea
Human heavy chain
Anti-melanoma anti
Anti-melanoma anti
Anti-idiocyte mon
Amino acid sequenc
Anti-idiocyte mon
Human novel protei
Human heavy chain
Human heavy chain
Human TF anti-Idio
Humanised anti-Ido
scFv-B1 antibody
Consensus humanise
Internalising anti
Human HIV-1 monocl
Human TF anti-Idio
Human anti-tissue
Anti-idiocyte mon
Anti-melanoma anti
Heavy chain variab
Peptide sequence 0

PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

XX Example 2; Page 41; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody LT28
CC heavy chain sequence.

XX Sequence 108 AA;

Query Match 100.0%; Score 572; DB 22; Length 108;

Best Local Similarity 100.0%; Pred. No. 5,3e-46;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVOPGSLRLSCAAGFTFSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFTI 60
DB 1 LVPGGSLRLSCAAGFTFSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFTI 60

QY 61 SRDNSKNTLYIQMNSLRADPTAVYVCARDDDVDYFDWGRGTMTVTS 108
DB 61 SRDNSKNTLYIQMNSLRADPTAVYVCARDDDVDYFDWGRGTMTVTS 108

RESULT 2

ID AAG65354 standard; protein: 118 AA.

XX AAG65354;

XX 30-NOV-2001 (first entry)

XX Anti-IL-18 antibody LT28 heavy chain sequence.

XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.

XX Homo sapiens.

XX WO200158956-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04170.

XX 10-FEB-2000; 2000US-0181608.

XX (BADI) BASF AG.

PI Ghayur T, Dixon RM, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shortrock CP, Thompson JE;
PI Lennard SN;

DR WPI: 2001-550020/61.
DR N-PSDB; AAH47513.

PT Novel antibodies and compounds capable of binding to human

PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

XX Claim 1; Page 89; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody LT28
CC heavy chain sequence.

XX Sequence 118 AA;

Query Match 100.0%; Score 572; DB 22; Length 118;

Best Local Similarity 100.0%; Pred. No. 5,9e-46;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVOPGSLRLSCAAGFTFSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFTI 60
DB 1 LVPGGSLRLSCAAGFTFSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFTI 70

QY 61 SRDNSKNTLYIQMNSLRADPTAVYVCARDDDVDYFDWGRGTMTVTS 108
DB 71 SRDNSKNTLYIQMNSLRADPTAVYVCARDDDVDYFDWGRGTMTVTS 118

RESULT 3

ID AAG65320 standard; protein: 235 AA.

XX AAG65320;

XX 30-NOV-2001 (first entry)

XX Anti-IL-18 antibody LT28 sequence.

XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.

XX Homo sapiens.

XX WO200158956-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04170.

XX 10-FEB-2000; 2000US-0181608.

XX (BADI) BASF AG.

PI Ghayur T, Dixon RM, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shortrock CP, Thompson JE;
PI Lennard SN;

DR WPI: 2001-550020/61.

PT Novel antibodies and compounds capable of binding to human
PT interleukin-18 useful for treating, e.g., inflammatory disorders,

PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

XX Examples: Page 79-80; 91pp; English.

CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 1728
CC comprising the heavy chain and light chain sequences joined by a linker.

XX Sequence 235 AA:

Query Match 100.0%; Score 572; DB 22; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.3e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVPGGSLRLSCAAGFTFSYAMSWVROAPGKGLVWVAISGSGSTYYADSVKGRFTI 60

Db 1 LVPGGSLRLSCAAGFTFSYAMSWVROAPGKGLVWVAISGSGSTYYADSVKGRFTI 60

QY 61 SRDMSKNTLYLQNSLRADTAVYVCARDDDDYDFDYGRTWTVSS 108

Db 61 SRDMSKNTLYLQNSLRADTAVYVCARDDDDYDFDYGRTWTVSS 108

RESULT 4

AAW27553 standard; Protein; 120 AA.

XX AAW27553;

XX 23-JAN-1998 (first entry)

XX Human Ab heavy chain variable region VH3 consensus.

XX Human; antibody; preparation; library; VH3; variable region;

XX heavy chain; consensus.

XX Homo sapiens.

XX MO9708320-A1.

XX 06-MAR-1997.

XX 19-AUG-1996; 96WO-EP03647.

XX 18-AUG-1995; 95EP-0113021.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.

XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;

XX WPI; 1997-179277/16.

XX N-PSDB; AAT87951.

XX Preparation of human derived antibody gene library - using synthetic

XX consensus sequences, and signal consensus antibody gene as universal

XX framework for highly diverse antibody libraries

XX Example 1; Fig 5D; 436pp; English.

XX The present sequence is the human antibody heavy chain
CC variable region synthetic sequence VH3, used in the preparation of
CC a human derived antibody gene library.

XX Sequence 120 AA:

Query Match 90.4%; Score 517; DB 18; Length 120;
Best Local Similarity 91.8%; Pred. No. 7.9e-41;
Matches 101; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 LVPGGSLRLSCAAGFTFSYAMSWVROAPGKGLVWVAISGSGSTYYADSVKGRFTI 60

Db 1 LVPGGSLRLSCAAGFTFSYAMSWVROAPGKGLVWVAISGSGSTYYADSVKGRFTI 70

QY 61 SRDMSKNTLYLQNSLRADTAVYVCAR--DDDDYDFDYGRTWTVSS 108

Db 71 SRDMSKNTLYLQNSLRADTAVYVCARWGGGdYamdywgggdlvss 120

RESULT 5

AAW27560 standard; Protein; 261 AA.

XX AAW27560;

XX 23-JAN-1998 (first entry)

XX Consensus single chain fragment VH3-V-kappa-2.

XX Human; antibody; preparation; library; VH3; variable region;

XX light chain; heavy chain; V-kappa-2; single chain; consensus.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..21

XX Peptide /label= sig_peptide

XX Peptide /label= mat_peptide

XX MO9708320-A1.

XX 06-MAR-1997.

XX 19-AUG-1996; 96WO-EP03647.

XX 18-AUG-1995; 95EP-0113021.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMERUNG MBH.

XX Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;

XX WPI; 1997-179277/16.

XX N-PSDB; AAT87958.

XX Preparation of human derived antibody gene library - using synthetic

XX consensus sequences, and signal consensus antibody gene as universal

XX framework for highly diverse antibody libraries

XX Example 2; Fig 8; 436pp; English.

XX The present sequence is the consensus single chain fragment

XX VH3-V-kappa-2, which comprises the human antibody

XX heavy and light chain variable region consensus sequences VH3 and

XX V-kappa-2, was used in the preparation of a human derived antibody

Query Match 90.4%; Score 517; DB 18; Length 281;
 Best Local Similarity 91.8%; Pred. No. 2e-40; Mismatches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 LVPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVAISGGSTYYADSVKGRFTI 60
 Db 36 LVqpgsrlrlscaasgftssyamswwrqpqkglewvsaisgsgstyadsvkgrftl 95
 OY 61 SROSKNTLYLQMSLRAEDTAVVYCCAR--DDDDYDPDYGRGTMTYVSS 108
 Db 96 strdnskntlylqmslraedtavvycarwgddgfyandymwggtlvtvss 145

RESULT 6
 AAE07014
 ID AAE07014 standard; protein: 128 AA.
 AC AAE07014;
 XX 16-OCT-2001 (first entry)
 DE Human heavy chain variable (VH) region, 038062.
 XX
 KW Human: humanised antibody: CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; atherosclerosis; restenosis; asthma;
 KW anaplasia; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention; ID9 antibody;
 KW neointimal hyperplasia; VH; heavy chain variable region.
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH 31..35
 FT /label= CDR1
 FT /note= "Complementarity determining region 1"
 FT 50..66
 FT /label= CDR2
 FT /note= "Complementarity determining region 2"
 FT 99..117
 FT /label= CDR3
 FT /note= "Complementarity determining region 3"
 FT Misc-difference 109
 FT /label= Unknown
 XX

PN WO200157226-A1.
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-US03537.
 XX
 PR 03-FEB-2000; 2000US-0497625.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX WPI; 2001-488888/53.
 DR
 XX Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT
 XX Disclosure; Page 168; 183p; English.
 PS
 XX The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The

CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherosclerosis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR2 mediated
 CC disease. They are also useful for treating allergy, anaplasia,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is human heavy chain variable (VH) region, 038062.
 XX

SO Sequence 128 AA;

Query Match 90.0%; Score 515; DB 22; Length 128;
 Best Local Similarity 85.6%; Pred. No. 1.3e-40; Mismatches 10; Conservative 3; Mismatches 4; Indels 10; Gaps 1;

QY 1 LVPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVAISGGSTYYADSVKGRFTI 60
 Db 11 LVqpgsrlrlscaasgftssyamswwrqpqkglewvsaisgsgstyadsvkgrftl 70
 OY 61 SROSKNTLYLQMSLRAEDTAVVYCCARDDDDYF-----DYGRGTMTYVSS 108
 Db 71 strdnskntlylqmslraedtavvycakdrnrdtwsqxyyygmddwggtlvtvss 128

RESULT 7
 AAM13524
 ID AAM13524 standard; protein: 140 AA.
 AC AAM13524;
 XX 28-OCT-1997 (first entry)
 DE Anti-melanoma antibody heavy chain clone V86.
 XX
 KW Human: monoclonal antitumour antibody; peripheral blood lymphocyte;
 KW cancer; tumorigenesis; anticancer vaccine.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH 31..35
 FT /label= CDR1
 FT 50..66
 FT /label= CDR2
 FT 99..113
 FT /label= CDR3
 XX

PN WO9702479-A2.
 PD 23-JAN-1997.
 XX
 PF 28-JUN-1996; 96WO-IB01032.
 XX
 PR 30-JUN-1995; 95US-0497647.
 XX
 XX (UYA) UNIV YALE.
 PA
 PI Cai X, Garen A;
 XX WPI; 1997-109061/10.
 DR
 XX Prodn. of human monoclonal anti-tumour antibodies - by screening a

PT fusion phage library produced using peripheral blood lymphocytes
 PT from a cancer patient
 PS Claim 19: Page 62: 82pp; English.
 CC A process for isolating and synthesizing human monoclonal anti-tumour
 CC antibodies has been produced. The process involves: (a) constructing at
 CC least one fusion phage library from the peripheral blood lymphocytes
 CC (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in
 CC the phage library in a binding assay with cultured tumour cells of the
 CC same type as the patient's tumour; (c) removing extraneous antibodies by
 CC absorption against normal human cells; (d) cloning the phage selected in
 CC step (b) and (c); (e) assaying the specificity of the cloned phage by
 CC incubating the phage with at least two types of cultured normal cells;
 CC and (f) further testing the specificity of cloned phage that do not bind
 CC to either cell line of cultured normal cells in further binding assays
 CC to cultured tumour cells derived from more than one other tumour that is
 CC not the patient's tumour. The present sequence represents a human heavy
 CC chain antibody, from an scfv antibody fusion phage library, produced by
 CC a method as described above. The antibodies produced can be used for
 CC diagnostic and therapeutic applications and for isolating tumour
 CC antigens for studying tumourigenesis or for use as anti-cancer vaccines.
 CC The human antibodies have low immunogenicity in humans compared to
 CC murine monoclonal antibodies (Mabs). Since the antibodies are isolated
 CC from fusion phage libraries, their affinity and specificity for a
 CC tumour cell line can be improved by genetic manipulations.
 CC
 XX Sequence 140 AA;

Query Match 90.0%; Score 515; DB 18; Length 140;
 Best Local Similarity 87.7%; Pred. No. 1.4e-40;
 Matches 100; Conservative 4; Mismatches 4; Indels 6; Gaps 1;

OY 1 LVQPGSLRLSCAAGFTFSSYAMSWVRQAPGKLEWNSAISGSGSTYYADSVKGRFTI 60
 |||||
 DB 11 LVQPGSLRLSCAAGFTFSSYAMSWVRQAPGKLEWNSAISGSGSTYYADSVKGRFTI 70
 |||||

OY 61 SRDNRKNTLYLQNSLRADPTAVYYCAR-----DDDDYDFDYGKGMVTVSS 108
 |||||
 DB 71 SRDNRKNTLYLQNSLRADPTAVYYCAR-----DDDDYDFDYGKGMVTVSS 124
 |||||

RESULT 8

AAU14320
 ID AAU14320 standard; Protein: 313 AA.

AC AAU14320;

DT 24-OCT-2001 (first entry)

DE Human novel protein #191.

XX Human; novel protein; Antianemic; osteopathic; antiinflammatory;
 KW immunomodulatory; cytoskeletal; neuroprotective; vulnerrary; nootropic;
 KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
 KW antibacterial; antiallergic; dermatological; haemostatic; antistimatic;
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KW tissue regeneration; immune disorder.

OS Homo sapiens.

XX WO200155437-A2.

XX 02-AUG-2001.

XX 25-JAN-2001: 2001WO-US02623.

XX 25-JAN-2000: 2000US-0491404.

XX (HYSB-) HYSBQ INC.

XX

PI Tang YT, Liu C, Dymnack RT;
 DR WPI: 2001-451939/48.
 DR N-PSDB: AAS22625.

PT Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage -
 PS Example 4: Page 630-631; 894pp; English.

CC The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicite an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.

SO Sequence 313 AA;

Query Match 89.6%; Score 512.5; DB 22; Length 313;
 Best Local Similarity 85.5%; Pred. No. 6e-40;
 Matches 100; Conservative 3; Mismatches 5; Indels 9; Gaps 1;

OY 1 LVQPGSLRLSCAAGFTFSSYAMSWVRQAPGKLEWNSAISGSGSTYYADSVKGRFTI 60
 |||||
 DB 71 LVQPGSLRLSCAAGFTFSSYAMSWVRQAPGKLEWNSAISGSGSTYYADSVKGRFTI 130
 |||||

OY 61 SRDNRKNTLYLQNSLRADPTAVYYCARDD-----DYDPYWGKGMVTVSS 108
 |||||
 DB 131 SRDNRKNTLYLQNSLRADPTAVYYCARDD-----DYDPYWGKGMVTVSS 187
 |||||

RESULT 9

AAE07029
 ID AAE07029 standard; Protein: 121 AA.

AC AAE07029;

DT 16-OCT-2001 (first entry)

DE Human heavy chain variable (VH) region, VH clone 41.

XX Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytoskeletal; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; stenosis; allograft rejection;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention; ID9 antibody;
 KW neonatal hyperplasia; VH; heavy chain variable region.

OS Homo sapiens.

CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
CC a vessel in a mammal, preferably associated with vascular intervention.
CC The present sequence is human heavy chain variable (VH) region, 038064.
XX

XX The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2
CC (CCR2), comprising an antigen binding region of non-human origin
CC and at least a portion of an immunoglobulin of human origin. The
CC humanised antibodies are useful for inhibiting the interaction of
CC a cell expressing CCR2. They are useful for inhibiting or treating
CC HIV infection. The proteins of the invention are useful for inhibiting
CC leukocyte trafficking, for treating CCR2-mediated disorders such as
CC inflammatory disorder, autoimmune disorders such as rheumatoid
CC arthritis and multiple sclerosis, atherosclerosis and arteriosclerosis,
CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
CC and in the manufacture of a medicament for treating CCR2-mediated
CC disease. They are also useful for treating allergy, anaphylaxis,
CC malignancy, chronic and acute inflammation, histamine and 19E-
CC mediated allergic reaction, shock, stenosis, allograft rejection,
CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
CC immune deficiency syndrome (AIDS), restenosis associated with vascular
CC intervention, including angioplasty and/or stent placement in a mammal.
CC Humanised antibodies are also useful for inhibiting narrowing of the
CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
CC a vessel in a mammal, preferably associated with vascular intervention.
CC The present sequence is human heavy chain variable (VH) region, 029764.

Query Match 89.4%; Score 511.5; DB 22; Length 125;

Best Local Similarity 87.0%; Pred. No. 2.7e-40;
Matches 100; Conservative 3; Mismatches 5; Indels 7; Gaps 1;

QY 1 LVPGGSLRLSCAAGTSSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFT 60
DB 11 LVPGGSLRLSCAAGTSSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFT 70

QY 61 SRDMSKNTLYLQMSLRADTAVYCARDDP-----YDFPYMGRTWVTVSS 108
DB 71 SRDMSKNTLYLQMSLRADTAVYCARDDP-----YDFPYMGRTWVTVSS 125

RESULT 11

AAE07026 standard; Protein; 124 AA.

AAE07026;

16-OCT-2001 (first entry)

Human heavy chain variable (VH) region, 029764.

Human: humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherosclerosis; arteriosclerosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
KW AIDS; inflammatory glomerulopathy; vascular intervention; ID9 antibody;
KW neointimal hyperplasia; VH; heavy chain variable region.

OS Homo sapiens.

Location/Qualifiers

Region

/label=CDR1
/note="Complementarity determining region 1"

Region

/label=CDR2
/note="Complementarity determining region 2"

Region

/label=CDR3
/note="Complementarity determining region 3"

WO200157226-A1.

09-AUG-2001.

02-FEB-2001; 2001WO-US03537.

03-FEB-2000; 2000US-0497625.

(MILL-) MILLENNIUM PHARM INC.

Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

WPI; 2001-48888/53.

Humanized immunoglobulin for treating a CC-chemokine receptor
2-mediated disorder in a patient, comprises a binding specificity for
CCR2, and a non-human antigen binding region and human immunoglobulin

Disclosure; Page 173; 183pp; English.

Sequence 124 AA:

Query Match 89.2%; Score 510; DB 22; Length 124;

Best Local Similarity 86.8%; Pred. No. 3.7e-40;
Matches 99; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

QY 1 LVPGGSLRLSCAAGTSSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFT 60
DB 11 LVPGGSLRLSCAAGTSSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFT 70

QY 61 SRDMSKNTLYLQMSLRADTAVYCARDDP-----DDDDYDFPYMGRTWVTVSS 108
DB 71 SRDMSKNTLYLQMSLRADTAVYCARDDP-----DDDDYDFPYMGRTWVTVSS 124

RESULT 12

AAW78432 standard; Protein; 122 AA.

AAW78432;

11-MAY-1999 (first entry)

Antibody heavy chain targeted to HER3 clone 18.

Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;
KW diagnosis; cancer; primer; PCR; amplification; diastrophic.

Synthetic.

WO9850431-A2.

12-NOV-1998.

30-APR-1998; 98WO-US08762.

24-JUN-1997; 97US-0050661.

02-MAY-1997; 97US-0850058.

(GETH) GENENTECH INC.

Arathoon R, Carter PJ, Merchant AM, Presta LG;

WPI; 1999-070091/06.

Selective preparation of multispecific antibodies - with
heteromultimeric heavy chain and common light chain components,
useful for, e.g. in vivo diagnosis of cancer

XX Example 4; Fig 5; 69pp; English.

CC This sequence represents the heavy chain variable region for an antibody
 CC that binds to the HER3 clone 18 protein. The sequence encoding the chain
 CC is generated by a new method for preparing a multispecific Ab comprising
 CC a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP
 CC comprises a multimerisation domain (MD) forming an interface positioned
 CC to interact with an interface of a MD of the extra PP; and (ii) the first
 CC and extra PPs each have a binding domain, which comprises a heavy chain
 CC and a light chain, where the variable light chains of the first and extra
 CC PPs comprise a common sequence. The method comprises: (a) culturing a
 CC host cell comprising nucleic acid encoding the first PP and extra PP, and
 CC the variable light chain, such that the nucleic acid is expressed; and
 CC (b) recovering the multispecific Ab from the culture. The method prepares
 CC heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins
 CC and Ab-immunoadhesin chimeras. The method allows for the enhanced
 CC formation of the desired heteromultimer relative to the undesired
 CC heteromultimers and homomultimers. The Abs can be used in immunoassays
 CC and for the in vitro or in vivo diagnosis of various diseases, such as
 CC cancer.

XX Sequence 122 AA;

Query Match 89.0%; Score 509; DB 20; Length 122;
 Best Local Similarity 88.4%; Pred. No. 4.5e-40;
 Matches 99; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 1 LVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATISGSGSTTYADSVKGRFTI 60
 |||
 Db 11 LVpggsalrlscaasgftfssyamswwrqpqgkglwvsaisgsgstyadsvkgrftl 70

QY 61 SRDNSKNTLYIQMNSLRADPTAVYYCARD---DDYDFDYGWGRGMVTYSS 108
 |||
 Db 71 srdsnktlylqmnrlraetlavyycaardngwldtgyfclwgrgmvtvss 122

RESULT 13

AAAY02472
 ID AAY02472 standard; Protein; 240 AA.

XX AC AAY02472;

XX DT 15-JUL-1999 (first entry)

XX DE A single chain antibody (ScFv).

KW Screening; functional polypeptide; ligand; non-functional;

KW enrichment; single chain antibody; ScFv.

XX OS Unidentified.

XX PN WO9920749-A1.

XX PD 29-APR-1999.

XX PF 20-OCT-1998; 98WO-GB03135.

XX PR 21-NOV-1997; 97US-0066729.

XX PR 20-OCT-1997; 97GB-0022131.

XX PR 13-NOV-1997; 97US-0065428.

XX PA (MED1-) MEDICAL RES COUNCIL.

XX PI Tomlinson I, Winter G;

XX DR WPI; 1999-288302/24.

XX DR N-PSDB; AAX36070.

XX PT Screening for functional polypeptides which bind a ligand

XX PS Disclosure; Fig 2; 67pp; English.

XX The specification describes a method for screening for functional
 CC polypeptides which bind a ligand. The method comprises contacting a
 CC repertoire of polypeptides with a generic ligand, and then screening
 CC selected functional polypeptides with a target ligand. The method
 CC permits the removal from a chosen repertoire of polypeptides, those
 CC which are non-functional, e.g. as a result of the introduction of
 CC frame-shift mutations, stop codons, folding mutants or expression
 CC mutants which would be or are incapable of binding to any target
 CC ligand. The method also permits the enrichment of a chosen repertoire
 CC of polypeptides for those polypeptides which are functional, well folded
 CC and highly expressed. The polypeptides obtained can be used in
 CC diagnostic, prophylactic and therapeutic procedures. The present
 CC sequence represents the single chain antibody (ScFv) that forms the
 CC basis of a library according to the invention.

XX Sequence 240 AA;

Query Match 89.0%; Score 509; DB 20; Length 240;
 Best Local Similarity 91.7%; Pred. No. 9.4e-40;
 Matches 100; Conservative 3; Mismatches 2; Indels 4; Gaps 2;

QY 1 LVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATISGSGSTTYADSVKGRFTI 60
 |||
 Db 11 LVpggsalrlscaasgftfssyamswwrqpqgkglwvsaisgsgstyadsvkgrftl 70

QY 61 SRDNSKNTLYIQMNSLRADPTAVYYCARD---DDYDFDYGWGRGMVTYSS 108
 |||
 Db 71 srdsnktlylqmnrlraetlavyyca---syaafdywgggtlvtvss 116

RESULT 14

AAAY15124
 ID AAY15124 standard; Protein; 240 AA.

XX AC AAY15124;

XX DT 07-FEB-2000 (first entry)

XX DE Anti-human CTLA-4 sFv.

KW Anti-human CTLA-4 sFv; single chain antibody; phage; human CTLA-4;

KW membrane-associated protein; ligand; activated T-cell; B7; CD28;

KW co-stimulatory signal; T-cell proliferation; xenograft; organ transplant;

KW xenograft-specific immunosuppression.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Region 116..130
 XX FT /label=Linker_region

XX PN WO9957266-A2.

XX PD 11-NOV-1999.

XX PF 30-APR-1999; 99WO-GB01350.

XX PR 30-APR-1998; 98GB-0009280.

XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX PI Lechler IR, Dorling A;

XX DR WPI; 2000-038815/03.

XX DR N-PSDB; AAZ28996.

XX PT Inhibiting T-cell mediated rejection of xenotransplanted organs

XX PS Claim 9; Fig 9; 43pp; English.

XX The present sequence is the anti-human CTLA-4 sFv. This is a membrane

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:45 ; Search time 84.18 Seconds
(without alignments)
31.337 Million cell updates/sec

Title: US-09-780-035-28

Perfect score: 572
Sequence: 1 LVDPGSLRLSCAASGFTFS.....DDDDYFDYWGRCMTVSS 108

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	517	90.4	120	4	US-09-025-769B-38 Sequence 38, Appl
2	517	90.4	120	4	US-09-025-769B-63 Sequence 63, Appl
3	517	90.4	281	4	US-09-025-769B-178 Sequence 178, Appl
4	515	90.0	140	4	US-08-983-607-32 Sequence 32, Appl
5	506.5	88.5	113	3	US-08-974-899-6 Sequence 6, Appl
6	505	88.3	122	2	US-07-934-373C-21 Sequence 21, Appl
7	505	88.3	122	3	US-08-437-642B-21 Sequence 21, Appl
8	503	87.9	122	5	PCT-US93-07832-21 Sequence 21, Appl
9	503	87.9	131	4	US-08-983-607-51 Sequence 51, Appl
10	503	87.9	131	4	US-08-983-607-28 Sequence 28, Appl
11	496	86.7	135	4	US-08-579-378A-20 Sequence 20, Appl
12	496	86.7	443	5	PCT-US96-13152-4 Sequence 4, Appl
13	493.5	86.3	125	2	US-08-428-197-1 Sequence 1, Appl
14	493.5	86.3	125	2	PCT-US93-10555-1 Sequence 1, Appl
15	492	86.0	116	4	US-08-983-607-36 Sequence 36, Appl
16	490	85.7	124	4	US-08-983-607-47 Sequence 47, Appl
17	488.5	85.4	117	4	US-08-983-607-46 Sequence 46, Appl
18	488	85.3	118	2	US-08-652-816A-12 Sequence 12, Appl
19	488	85.3	283	4	US-09-420-592A-6 Sequence 6, Appl
20	485.5	84.9	117	4	US-09-025-769B-24 Sequence 24, Appl
21	480.5	84.0	125	1	US-08-478-039-99 Sequence 99, Appl
22	480.5	84.0	125	1	US-08-476-349A-99 Sequence 99, Appl
23	479.5	83.8	120	5	US-08-428-197-20 Sequence 20, Appl
24	479.5	83.8	120	5	PCT-US93-10555-20 Sequence 20, Appl
25	479	83.7	144	1	US-08-026-320A-2 Sequence 2, Appl
26	478.5	83.7	120	4	US-08-428-197-22 Sequence 22, Appl
27	478.5	83.7	120	5	PCT-US93-10555-22 Sequence 22, Appl

28	478	83.6	123	2	US-08-428-197-38 Sequence 38, Appl
29	478	83.6	123	5	PCT-US93-10555-38 Sequence 38, Appl
30	477.5	83.5	123	2	US-08-665-202-30 Sequence 30, Appl
31	476.5	83.3	120	2	US-08-428-197-24 Sequence 24, Appl
32	476.5	83.3	120	2	US-08-428-197-26 Sequence 26, Appl
33	476.5	83.3	120	2	US-08-428-197-28 Sequence 28, Appl
34	476.5	83.3	120	2	US-08-428-197-30 Sequence 30, Appl
35	476.5	83.3	120	2	US-08-428-197-32 Sequence 32, Appl
36	476.5	83.3	120	2	US-08-428-197-40 Sequence 40, Appl
37	476.5	83.3	120	5	PCT-US93-10555-24 Sequence 24, Appl
38	476.5	83.3	120	5	PCT-US93-10555-26 Sequence 26, Appl
39	476.5	83.3	120	5	PCT-US93-10555-30 Sequence 30, Appl
40	476.5	83.3	120	5	PCT-US93-10555-32 Sequence 32, Appl
41	476.5	83.3	120	5	PCT-US93-10555-40 Sequence 40, Appl
42	476.5	83.3	120	5	PCT-US93-10555-40 Sequence 40, Appl
43	473	82.7	245	1	US-08-918-148-75 Sequence 75, Appl
44	471.5	82.4	119	1	US-07-988-925-11 Sequence 11, Appl
45	471.5	82.4	119	2	US-08-362-780-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-38
Sequence 38, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-38
Query Match 90.4%, Score 517, DB 4, Length 120;
Best Local Similarity 91.8%, Pred. No. 3,7e+45;

REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 122 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-07-934-373C-21

Query Match 88.3%; Score 505; DB 2; Length 122;
 Best Local Similarity 87.5%; Pred. No. 6e-44;
 Matches 98; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 LVQPGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVAISGSGSTYYADSVKGRFTI 60
 |||
 DB 11 LVQPGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVAISGSGSTYYADSVKGRFTI 70
 |||
 QY 61 SRDNSKNTLYLQMNSLRAEDTAVYYCARGVYSLGSLYDWGGTLVTYSS 108
 |||
 DB 71 SRDNSKNTLYLQMNSLRAEDTAVYYCARGVYSLGSLYDWGGTLVTYSS 122
 |||

RESULT 7

US-08-437-642B-21
 Sequence 21, Application US/08437642B
 Patent No. 6054297

GENERAL INFORMATION:
 APPLICANT: Paul J. Carter
 APPLICANT: Leonard G. Presta
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/437,642B
 FILING DATE: 09-May-1995

CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/934373
 FILING DATE: 21-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/146206
 FILING DATE: 17-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P2C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 122 amino acids

TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-437-642B-21

Query Match 88.3%; Score 505; DB 3; Length 122;
 Best Local Similarity 87.5%; Pred. No. 6e-44;
 Matches 98; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 LVQPGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVAISGSGSTYYADSVKGRFTI 60
 |||
 DB 11 LVQPGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVAISGSGSTYYADSVKGRFTI 70
 |||
 QY 61 SRDNSKNTLYLQMNSLRAEDTAVYYCARGVYSLGSLYDWGGTLVTYSS 108
 |||
 DB 71 SRDNSKNTLYLQMNSLRAEDTAVYYCARGVYSLGSLYDWGGTLVTYSS 122
 |||

RESULT 8

PCT-US93-07832-21
 Sequence 21, Application PC/TUS9307832

GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 APPLICANT: Leonard G. Presta
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/07832
 FILING DATE: 19930820

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/934373
 FILING DATE: 21-AUG-1992
 ATTORNEY/AGENT INFORMATION:
 NAME:

REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 709P2PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE:

TELEFAX: 415/952-9881
 TELEFAX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 122 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 PCT-US93-07832-21

Query Match 88.3%; Score 505; DB 5; Length 122;
 Best Local Similarity 87.5%; Pred. No. 6e-44;
 Matches 96; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 LVQPGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVAISGSGSTYYADSVKGRFTI 60
 |||
 DB 11 LVQPGSLRLSCAASGFTSSYAMSWVRQAPGKLEWVAISGSGSTYYADSVKGRFTI 70
 |||

QY 61 SRNSKNTLYLQMSLSRAEDTAVYTCARDDDDYD---FDYMGRTWTVSS 108
 Db 71 SRNSKNTLYLQMSLSRAEDTAVYTCARGVYSLSGLYDYGQGLTVTVSS 122

RESULT 9

US-08-983-607-51
 ; Sequence 51, Application US/08983607
 ; Patent No. 6140470
 ; GENERAL INFORMATION:
 ; APPLICANT: Alan Garen
 ; APPLICANT: Xiaohong Cai
 ; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
 ; TITLE OF INVENTION: bodies
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Department of Molecular Biophysics
 ; ADDRESSEE: and Biochemistry, Yale University
 ; STREET: 266 Whitney Avenue
 ; CITY: New Haven
 ; STATE: Connecticut
 ; COUNTRY: United States of America
 ; ZIP: 06520-8114
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" 1.44 Mb diskette
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: Word Processing
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/983,607
 ; FILING DATE: April 27, 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/IB96/01032
 ; FILING DATE: June 28, 1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mary M. Krinsky
 ; REGISTRATION NUMBER: 32423
 ; REFERENCE/DOCKET NUMBER: OCR-679
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 203-773-9544
 ; TELEFAX: 203-773-1183
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 124 residues
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:
 ; DESCRIPTION: polypeptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens (melanoma patient
 ; INDIVIDUAL ISOLATE: immunized with autologous tumor cells)
 ; INDIVIDUAL ISOLATE: peripheral blood lympho-
 ; IMMEDIATE SOURCE:
 ; LIBRARY: VH antibodies obtained from fuses
 ; CLONE: E-13
 ; FEATURE:
 ; NAME/KEY: heavy chain
 ; US-08-983-607-51

Query Match 87.9%; Score 503; DB 4; Length 124;
 Best Local Similarity 87.5%; Pred. No. 9.8e-44;
 Matches 98; Conservative 3; Mismatches 5; Indels 6; Gaps 1;

QY 1 LVOPGSLRLSCAASGTFSSYAMSVROAPGKLEWVSAISGSGSTYYADSVKGRFTI 60
 Db 11 LVOPGSLRLSCAASGTFSSYAMSVROAPGKLEWVSAISGSGSTYYADSVKGRFTI 70

QY 61 SRNSKNTLYLQMSLSRAEDTAVYTCARDDDDYD---DDDDYDYPGRTWTV 106
 Db 71 SRNSKNTLYLQMSLSRAEDTAVYTCARGWGLRGEDGYVDVWGKTKTV 122

RESULT 10

US-08-983-607-28
 ; Sequence 28, Application US/08983607
 ; Patent No. 6140470
 ; GENERAL INFORMATION:
 ; APPLICANT: Alan Garen
 ; APPLICANT: Xiaohong Cai
 ; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
 ; TITLE OF INVENTION: bodies
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Department of Molecular Biophysics
 ; ADDRESSEE: and Biochemistry, Yale University
 ; STREET: 266 Whitney Avenue
 ; CITY: New Haven
 ; STATE: Connecticut
 ; COUNTRY: United States of America
 ; ZIP: 06520-8114
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" 1.44 Mb diskette
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: Word Processing
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/983,607
 ; FILING DATE: April 27, 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/IB96/01032
 ; FILING DATE: June 28, 1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mary M. Krinsky
 ; REGISTRATION NUMBER: 32423
 ; REFERENCE/DOCKET NUMBER: OCR-679
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 203-773-9544
 ; TELEFAX: 203-773-1183
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 131 residues
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:
 ; DESCRIPTION: polypeptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens (melanoma patient immu-
 ; INDIVIDUAL ISOLATE: nized with autologous tumor cells)
 ; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
 ; IMMEDIATE SOURCE:
 ; LIBRARY: DM414 scFv antibodies obtained from
 ; CLONE: V13
 ; FEATURE:
 ; NAME/KEY: heavy chain
 ; US-08-983-607-28

Query Match 87.9%; Score 503; DB 4; Length 131;
 Best Local Similarity 91.7%; Pred. No. 1e-43;
 Matches 99; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 LVOPGSLRLSCAASGTFSSYAMSVROAPGKLEWVSAISGSGSTYYADSVKGRFTI 60
 Db 11 LVOPGSLRLSCAASGTFSSYAMSVROAPGKLEWVSAISGSGSTYYADSVKGRFTI 70

QY 61 SRDNKNTLYLQMSLRAEDTAVYYCARDDDYDFDYGRTMTVYSS 108
|||||
Db 71 SRDNKNTLYLQMSLRAEDTAVYYCAK--GVAFEDYWGQGTPTVYSS 116

RESULT 11
US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: CO. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-20

Query Match 86.7%; Score 496; DB 4; Length 135;
Best Local Similarity 88.9%; Pred. No. 5.5e-43;
Matches 96; Conservative 7; Mismatches 3; Indels 2; Gaps 2;

QY 1 LVOPGSLRLSCAASGFTFSYAMSVVRQAPGKGLEWYSAISGSGSTYYADSVKGRFTI 60
|||||
Db 30 LVOPGSLRLSCAASGFTFSYAMSVVRQAPGKGLEWYSAIS-IGGSTIYDPDSVKGRFTI 88
QY 61 SRDNKNTLYLQMSLRAEDTAVYYCARDDDYDFDYGRTMTVYSS 108
|||||
Db 89 SRDNKNTLYLQMSLRAEDTAVYYCARDYDGY-FDYWGQGTLYTVYSS 135

RESULT 12
PCT-US96-13152-4

; Sequence 4, Application PCT/US9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-DEC-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-AUG-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-SEP-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-4

Query Match 86.7%; Score 496; DB 5; Length 443;
Best Local Similarity 88.9%; Pred. No. 2.2e-42;
Matches 96; Conservative 7; Mismatches 3; Indels 2; Gaps 2;

QY 1 LVOPGSLRLSCAASGFTFSYAMSVVRQAPGKGLEWYSAISGSGSTYYADSVKGRFTI 60
|||||
Db 11 LVOPGSLRLSCAASGFTFSYAMSVVRQAPGKGLEWYSAIS-IGGSTIYDPDSVKGRFTI 69
QY 61 SRDNKNTLYLQMSLRAEDTAVYYCARDDDYDFDYGRTMTVYSS 108
|||||
Db 70 SRDNKNTLYLQMSLRAEDTAVYYCARDYDGY-FDYWGQGTLYTVYSS 116

RESULT 13
US-08-428-197-1
; Sequence 1, Application US/08428197
; Patent No. 5891438
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONTIGATES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500


```

: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/428,197
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/10555
: FILING DATE: 29-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Howells, Stacy L.
: REGISTRATION NUMBER: 34,842
: REFERENCE/DOCKET NUMBER: FD-2630
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 455-5100
: TELEFAX: (619) 455-5110
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 125 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: IMMEDIATE SOURCE:
: CLONE: 18/2
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..125
: US-08-428-197-1

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Query Match      86.3%; Score 493.5; DB 2; Length 125;
Best Local Similarity 85.2%; Pred. No. 8.9e-43;
Matches 98; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

QY 1 LVOPGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFTI 60
   |||
DB 11 LVOPGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFTI 70
   |||

QY 61 SRDNSKNTLYLQMSLRADPTAVYYCARDDDYD-----FDYWGRTMVTYSS 108
   |||
DB 71 SRDNSKNTLYLQMSLRADPTAVYYCTKGQVLYYSGSYHMFDPWGQGLTVTVSS 125
   |||

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```

RESULT 14
PCT-US93-10555-1
: Sequence 1, Application PC/TUS9310555
: GENERAL INFORMATION:
: APPLICANT: SILVERMAN, GREGG J.
: TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
: TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
: TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND COMDUGATES
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Spensley Horn Judas & Lubitz
: STREET: 1880 Century Park East - Suite 500
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/10555
: FILING DATE: 29-OCT-1993
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Howells, Stacy L.
: REGISTRATION NUMBER: 34,842
: REFERENCE/DOCKET NUMBER: FD-2630
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 455-5100
: TELEFAX: (619) 455-5110
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 125 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: IMMEDIATE SOURCE:
: CLONE: 18/2
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..125
: PCT-US93-10555-1

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Query Match      86.3%; Score 493.5; DB 5; Length 125;
Best Local Similarity 85.2%; Pred. No. 8.9e-43;
Matches 98; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

QY 1 LVOPGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFTI 60
   |||
DB 11 LVOPGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVAISGSGSTYYADSVKGRFTI 70
   |||

QY 61 SRDNSKNTLYLQMSLRADPTAVYYCARDDDYD-----FDYWGRTMVTYSS 108
   |||
DB 71 SRDNSKNTLYLQMSLRADPTAVYYCTKGQVLYYSGSYHMFDPWGQGLTVTVSS 125
   |||

```

```

RESULT 15
US-08-983-607-36
: Sequence 36, Application US/08983607
: Patent No. 6140470
: GENERAL INFORMATION:
: APPLICANT: Xiahong Cai
: TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
: TITLE OF INVENTION: bodies
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Department of Molecular Biophysics
: ADDRESS: and Biochemistry, Yale University
: STREET: 266 Whitney Avenue
: CITY: New Haven
: STATE: Connecticut
: COUNTRY: United States of America
: ZIP: 06520-8114
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" 1.44 Mb diskette
: OPERATING SYSTEM: MS DOS
: SOFTWARE: Word Processing
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/983,607
: FILING DATE: April 27, 1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/IB96/01032
: FILING DATE: June 28, 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Mary M. Kinsky
: REGISTRATION NUMBER: 32423

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:47 ; Search time 84.18 Seconds

(without alignments)
32,208 Million cell updates/sec

Title: US-09-780-035-29

Perfect score: 580

Sequence: 1 QSVLTQPPSASGTGQRTVYI.....MDDSLSGFVGGGKTLVIG 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/6CTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	533	91.9	111	1	US-08-264-093-6
2	521	89.8	112	4	US-09-025-769B-18
3	515	88.8	113	1	US-08-211-202-113
4	513	88.4	109	4	US-09-240-274-59
5	513	88.4	111	2	US-08-665-202-40
6	511	88.1	109	4	US-09-240-274-55
7	510	87.9	111	2	US-08-665-202-43
8	508	87.6	109	4	US-09-240-274-57
9	508	87.6	111	2	US-08-983-607-23
10	505	87.1	111	2	US-08-665-202-36
11	505	87.1	258	4	US-08-665-202-5
12	505	87.1	282	4	US-09-420-592A-7
13	504.5	87.0	112	2	US-08-665-202-39
14	501	86.4	110	4	US-09-240-274-60
15	499	86.0	111	4	US-08-983-607-21
16	496	85.5	113	1	US-08-211-202-114
17	494	85.2	111	2	US-08-665-202-42
18	492	84.8	113	1	US-08-211-202-112
19	491	84.7	235	4	US-09-049-672A-12
20	483	83.3	111	4	US-08-983-607-21
21	482	83.1	109	4	US-09-240-274-56
22	481	82.9	109	4	US-09-240-274-54
23	479.5	82.7	236	4	US-09-049-672A-7
24	478	82.4	111	1	US-08-107-669D-4
25	478	82.4	111	1	US-08-472-788A-4
26	478	82.4	111	2	US-08-477-531B-4
27	478	82.4	111	2	US-08-082-842A-4

28	478	82.4	111	2	US-08-665-202-41	Sequence 41, Appl
29	475.5	82.0	106	1	US-08-488-113B-152	Sequence 152, App
30	475.5	82.0	106	1	US-08-477-484B-152	Sequence 152, App
31	475.5	82.0	106	2	US-08-646-360-152	Sequence 152, App
32	475.5	82.0	106	4	US-08-839-765-152	Sequence 152, App
33	475.5	82.0	106	4	US-09-136-389-152	Sequence 152, App
34	475	81.9	98	1	US-08-211-202-111	Sequence 111, App
35	475	81.9	98	2	US-08-665-202-38	Sequence 38, App
36	473	81.6	109	4	US-09-025-769B-32	Sequence 32, Appl
37	473	81.6	109	4	US-09-025-769B-51	Sequence 51, Appl
38	472	81.4	110	1	US-07-942-245-26	Sequence 26, Appl
39	469.5	80.9	106	1	US-08-107-669D-16	Sequence 16, Appl
40	469.5	80.9	106	1	US-08-472-788A-16	Sequence 16, Appl
41	469.5	80.9	106	2	US-08-477-531B-16	Sequence 16, Appl
42	469.5	80.9	106	2	US-08-082-842A-16	Sequence 16, Appl
43	463	79.8	109	4	US-09-240-274-180	Sequence 180, App
44	461	79.5	111	4	US-08-983-607-35	Sequence 35, Appl
45	460.5	79.4	310	4	US-09-079-029-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-264-093-6
Sequence 6, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2A7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 MB storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-6

Query Match 91.9%; Score 533; DB 1; Length 111;
Best Local Similarity 91.9%; Pred. No. 2.2e+40;
Matches 102; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 QSVLTQPPSASGTGQRTVYI.....MDDSLSGFVGGGKTLVIGNDPQSGVP 60
|||||

Db 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGTNYNWITQLPCTAPKVLITSNRPPSGVP 60
 QY 61 DRFSGSKSGTSASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLTVLG 111
 Db 61 DRFSGSKSGTSASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLTVLG 111

RESULT 2
 US-09-025-769B-18
 Sequence 18, Application US/09025769B
 Patent No. 6300064

GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 APPLICANT: Pack, Peter
 APPLICANT: 1199, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Moroney, Simon
 APPLICANT: Plueckhuhn, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-025-769B-18

Query Match 89.8%; Score 521; DB 4; Length 112;
 Best Local Similarity 90.1%; Pred. No. 2.5e-39;
 Matches 100; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMWYQQLPGTAPKLLIYGNDRPSGVP 60
 Db 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMWYQQLPGTAPKLLIYGNDRPSGVP 60
 QY 61 DRFSGSKSGTSASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLTVLG 111
 Db 61 DRFSGSKSGTSASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLTVLG 111

RESULT 3
 US-08-211-202-113
 Sequence 113, Application US/08211202
 Patent No. 5565332
 GENERAL INFORMATION:

APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
 APPLICANT: BATER, Michael
 APPLICANT: JESPEERS, Laurent Stephane Anne Therese
 APPLICANT: WINTER, Gregory Paul
 TITLE OF INVENTION: Production of chimeric antibodies - a
 TITLE OF INVENTION: combinatorial approach
 NUMBER OF SEQUENCES: 144
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606-6402

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/211,202
 FILING DATE: 23-SEP-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9120252.3
 FILING DATE: 23-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9120377.8
 FILING DATE: 25-SEP-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206318.9
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/00883
 FILING DATE: 15-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 28111/31960
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 113 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-211-202-113

Query Match 88.8%; Score 515; DB 1; Length 113;
 Best Local Similarity 91.2%; Pred. No. 8.5e-39;
 Matches 103; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMWYQQLPGTAPKLLIYGNDRPSGVP 60
 Db 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMWYQQLPGTAPKLLIYGNDRPSGVP 60
 QY 61 DRFSGSKSGTSASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLTVLG 111
 Db 61 DRFSGSKSGTSASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLTVLG 113

RESULT 4
 US-09-240-274-59
 Sequence 59, Application US/09240274
 Patent No. 6255455

```

: GENERAL INFORMATION:
: APPLICANT: Siegel, Donald L.
: TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
: TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
: FILE REFERENCE: 09596-4202
: CURRENT APPLICATION NUMBER: US/09/240,274
: CURRENT FILING DATE: 1999-01-29
: EARLIER APPLICATION NUMBER: 60/081,380
: EARLIER FILING DATE: 1998-04-10
: EARLIER APPLICATION NUMBER: 60/028,550
: EARLIER FILING DATE: 1996-10-11
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 59
: LENGTH: 109
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: anti-Rh(D) chain M02
US-09-240-274-59

Query Match      88.4%; Score 513; DB 4; Length 109;
Best Local Similarity 93.5%; Pred. No. 1.2e-38;
Matches 100; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQPPSASGTPGQRYTISCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDQPSGVPDRF 63
    |||
DB 3 LTQPPSASGTPGQRYTISCGSSSSNIGINAVMYQQLPGTAPKLLIYRNQRPSPGVPDRF 62
    |||

QY 64 SSKSGTSASLSAISGLQSEDEADYYCAAMDSDLSPVFGGKTLTVL 110
    |||
DB 63 SSKSGTSASLSAISGLQSEDEADYYCAAMDSDLSPVFGGKTLTVL 109
    |||

RESULT 5
US-08-665-202-40
: Sequence 40, Application US/08665202
: Patent No. 5977322
: GENERAL INFORMATION:
: APPLICANT: Marks, James D.
: APPLICANT: Schlier, Robert
: TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
: TITLE OF INVENTION: Tumor Antigens
: NUMBER OF SEQUENCES: 141
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/665,202
: FILING DATE: 13-JUN-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/000,238
: FILING DATE: 14-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/000,250
: FILING DATE: 15-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hunter, Tom
: REGISTRATION NUMBER: 38,498
: REFERENCE/DOCKET NUMBER: 02307E-061410
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
```

```

: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 40:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 111 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-665-202-40

Query Match      88.4%; Score 513; DB 2; Length 111;
Best Local Similarity 88.3%; Pred. No. 1.2e-38;
Matches 98; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSVLTQPPSASGTPGQRYTISCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDQPSGVP 60
    |||
DB 1 QSVLTQPPSASGTPGQRYTISCGSSSSNIGINAVMYQQLPGTAPKLLIYNDQPSGVP 60
    |||

QY 61 DFFSGSKSGTSASLSAISGLQSEDEADYYCAAMDSDLSPVFGGKTLTVL 111
    |||
DB 61 DFFSGSKSGTSASLSAISGLQSEDEADYYCAAMDSDLSPVFGGKTLTVL 111
    |||

RESULT 6
US-09-240-274-55
: Sequence 55, Application US/09240274
: Patent No. 6255455
: GENERAL INFORMATION:
: APPLICANT: Siegel, Donald L.
: TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
: TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
: FILE REFERENCE: 09596-4202
: CURRENT APPLICATION NUMBER: US/09/240,274
: CURRENT FILING DATE: 1999-01-29
: EARLIER APPLICATION NUMBER: 60/081,380
: EARLIER FILING DATE: 1998-04-10
: EARLIER APPLICATION NUMBER: 60/028,550
: EARLIER FILING DATE: 1996-10-11
: NUMBER OF SEQ ID NOS: 224
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 55
: LENGTH: 109
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: anti-Rh(D) chain I03
US-09-240-274-55

Query Match      88.1%; Score 511; DB 4; Length 109;
Best Local Similarity 92.5%; Pred. No. 1.8e-38;
Matches 99; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 LTQPPSASGTPGQRYTISCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDQPSGVPDRF 63
    |||
DB 3 LTQPPSASGTPGQRYTISCGSSSSNIGINAVMYQQLPGTAPKLLIYNDQPSGVPDRF 62
    |||

QY 64 SSKSGTSASLSAISGLQSEDEADYYCAAMDSDLSPVFGGKTLTVL 110
    |||
DB 63 SSKSGTSASLSAISGLQSEDEADYYCAAMDSDLSPVFGGKTLTVL 109
    |||

RESULT 7
US-08-665-202-43
: Sequence 43, Application US/08665202
: Patent No. 5977322
: GENERAL INFORMATION:
: APPLICANT: Marks, James D.
: APPLICANT: Schlier, Robert
: TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
: TITLE OF INVENTION: Tumor Antigens
: NUMBER OF SEQUENCES: 141
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-43

```

```

Query Match      87.9%; Score 510; DB 2; Length 111;
Best Local Similarity 89.2%; Pred. No. 2.3e-38;
Matches 99; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVMYQQLPGTAPKLLIYNDORPSGVP 60
DB 1 QSVLTQPPSVSAGRGQWVITSCGSSSSNIGNMYQQLPGTAPKLLIYDNKKRPSGVP 60
QY 61 DRESGSGTSASLAISGLQSEDEADYYCAAMDLSLGGVFGGKTLTVLG 111
DB 61 DRESGSGTSASLAISGLRSEDEADYYCAAMDLSLGGVFGGKTLTVLG 111

```

```

RESULT 8
US-09-240-274-57
Sequence 57, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 57
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens

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```

FEATURE:
OTHER INFORMATION: anti-Rh(D) chain I05
US-09-240-274-57

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Query Match      87.6%; Score 508; DB 4; Length 109;
Best Local Similarity 90.7%; Pred. No. 3.4e-38;
Matches 97; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 4 LTOPPSASGTPGQRTVITSCGSSSSNIGINAVMYQQLPGTAPKLLIYNDORPSGVPDRF 63
DB 3 LTOPPSASGTPGLVYITSCGSSSSNIGNMYQQLPGTAPKLLIYDNKKRPSGVPDRF 62
QY 64 SGSKSGTSASLAISGLQSEDEADYYCAAMDLSLGGVFGGKTLTVL 110
DB 63 SGSKSGTSASLAISGLQSEDEADYYCAWMDLSLGGVFGGKTLTVL 109

```

```

RESULT 9
US-08-983-607-23
Sequence 23, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
INDIVIDUAL ISOLATE: nized with autologous tumor cells)
IMMEDIATE SOURCE: peripheral blood lymphocytes
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: G57
FEATURE:

```


GENERAL INFORMATION:
APPLICANT: Filpula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whilow, Marc D.
TITLE OF INVENTION: NO. 63339661 Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.230001
CURRENT APPLICATION NUMBER: US/09/420,592A
CURRENT FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 282
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-420-592A-7

Query Match 87.1%; Score 505; DB 4; Length 282;
Best Local Similarity 87.4%; Pred. No. 1.7e-37;
Matches 97; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDRPSGVP 60
Db 1 QSVLTQPPSVSAAPGQKVTITSCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDRPSGVP 60
QY 61 DRESGSGTASLAISGLQSEDEADYYCAAMDLSLGPVGGGKTLLTVLG 111
Db 61 DRESGSGTASLAISGLQSEDEADYYCAAMDLSLGPVGGGKTLLTVLG 111

RESULT 13

US-08-665-202-39
Sequence 39, Application US/08665202
Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-39

Query Match 87.0%; Score 504.5; DB 2; Length 112;
Best Local Similarity 88.4%; Pred. No. 7.1e-38;
Matches 99; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDRPSGVP 60
Db 1 QSVLTQPPSVSAAPGQKVTITSCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDRPSGVP 60

QY 61 DRESGSGTASLAISGLQSEDEADYYCAAMDLSLGPVGGGKTLLTVLG 111
Db 61 DRESGSGTASLAISGLQSEDEADYYCAAMDLSLGPVGGGKTLLTVLG 112

RESULT 14

US-09-240-274-60
Sequence 60, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

OTHER INFORMATION: anti-Rh(D) chain M03
US-09-240-274-60

Query Match 86.4%; Score 501; DB 4; Length 110;
Best Local Similarity 91.6%; Pred. No. 1.4e-37;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 LTQPPSASGTPGQRTVITSCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDRPSGVPDRF 63
Db 3 LTQPPSASGTPGQRTVITSCGSSSSNIGINAVMYQQLPGTAPKLLIYNNDRPSGVPDRF 62

QY 64 SSGSGTASLAISGLQSEDEADYYCAAMDLSLGPVGGGKTLLTVL 110
Db 63 SSGSGTASLAISGLQSEDEADYYCAAMDLSLGPVGGGKTLLTVL 109

RESULT 15

US-08-983-607-27
Sequence 27, Application US/08983607
Patent No. 6140470

GENERAL INFORMATION:

APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:

2

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:17 ; Search time 245.49 Seconds
(without alignments)
50.223 Million cell updates/sec

Title: US-09-780-035-29

Sequence: 1 QSVTTPPSASGRFGKRVTL.....WDSLSGPRVGGKRLTVLG 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	580	100.0	111	22	AA65319
2	580	100.0	235	22	AA65320
3	566	97.6	111	22	AA65355
4	538	92.8	240	22	AA65358
5	538	92.8	244	22	AA65359
6	537	92.6	241	22	AA65360
7	536.5	92.5	118	22	AA65361
8	533	91.9	111	17	AA65362
9	533	91.9	111	20	AA65363
10	533	91.9	132	22	AA65364
11	533	91.9	236	22	AA65365

12	532	91.7	235	20	AA65366
13	527	90.9	111	22	AA65367
14	527	90.9	242	20	AA65368
15	524	90.3	244	20	AA65369
16	522	90.0	239	22	AA65370
17	519.5	89.6	109	21	AA65371
18	517	89.1	110	22	AA65372
19	516	89.0	153	21	AA65373
20	515	88.8	113	14	AA65374
21	514.5	88.7	240	21	AA65375
22	514.5	88.7	240	21	AA65376
23	514	88.6	243	22	AA65377
24	513.5	88.5	110	21	AA65378
25	513.5	88.5	242	21	AA65379
26	513	88.4	109	22	AA65380
27	513	88.4	111	18	AA65381
28	513	88.4	246	21	AA65382
29	511	88.1	109	22	AA65383
30	510	87.9	111	18	AA65384
31	508.5	87.7	248	22	AA65385
32	508	87.6	109	22	AA65386
33	508	87.6	111	18	AA65387
34	508	87.6	242	22	AA65388
35	507.5	87.5	109	21	AA65389
36	507.5	87.5	118	22	AA65390
37	505	87.1	258	18	AA65391
38	505	87.1	262	20	AA65392
39	504.5	87.0	112	18	AA65393
40	501	86.4	110	22	AA65394
41	499	86.0	111	18	AA65395
42	496	85.5	113	14	AA65396
43	495	85.3	237	22	AA65397
44	494	85.2	111	18	AA65398
45	492	84.8	113	14	AA65399

ALIGNMENTS

RESULT 1	AA65319	standard; protein; 111 AA.
ID	AA65319	
AC	AA65319	
DT	30-NOV-2001	(first entry)
DE	Anti-IL-18 antibody	IL28 light chain sequence.
KW	IL-18; interleukin-18; human; antibody; antineoplastic; cerebroprotective; neurotrophic; neurological; antineoplastic; antiparkinsonian; cardiant; immunosuppressive; antidepressant; neuroleptic; hepatotropic; IL28.	
OS	Homo sapiens.	
PN	WO200158956-A2.	
PD	16-AUG-2001.	
PF	09-FEB-2001; 2001WO-US04170.	
PR	10-FEB-2000; 2000US-0181608.	
PA	(BADI) BASF AG.	
PI	Chayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J; Duncan AR, Brocklehurst SM, Mankovich J, Shorrocks CP, Thompson JE; Leonard SN;	
PI	WPI; 2001-550020/61.	
DR	N-PSDB; AA647514.	
XX	Novel antibodies and compounds capable of binding to human	
PT		

Monoclonal antibody
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
Human TF anti-idio
Anti-platelet glyco
Anti-adipocyte mon
Human colon cancer
Human Vlamdbal-1-1
Anti-human CTLA-4
Anti-murine CTLA-4
Human TF anti-idio
Anti-platelet glyco
Anti-platelet glyco
Human anti-Rh(D) c
C6 human sfv antib
Anti-murine CTLA-4
Human anti-Rh(D) c
C6 human sfv antib
Novel human diagno
Human anti-Rh(D) c
Anti-melanoma ligh
Human TF anti-idio
Anti-platelet glyco
Human autoantibody
C6 human sfv antib
C6.5/218 single ch
C6 human sfv antib
Human anti-Rh(D) c
Anti-melanoma ligh
Human Vlamdbal-1-1
Novel human diagno
C6 human sfv antib
Human Vlamdbal-1-1

PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

PS Claim 36; Page 42; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody LT28
CC light chain sequence.

XX Sequence 111 AA;

Query Match 100.0%; Score 580; DB 22; Length 111;
Best Local Similarity 100.0%; Pred. No. 1,3e-38;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSVLTQPPSASGTPGQRTISCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDRPSGYP 60

Db 1 QSVLTQPPSASGTPGQRTISCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDRPSGYP 60

QY 61 DRFGSGSGTSASLAIISGLQSEDEADYCCAMPDLSGPFVGGGKTLTVLG 111

Db 61 DRFGSGSGTSASLAIISGLQSEDEADYCCAMPDLSGPFVGGGKTLTVLG 111

RESULT 2

AA655320 standard; protein; 235 AA.

AC AA655320;

DT 30-NOV-2001 (first entry)

DE Anti-IL-18 antibody LT28 sequence.

XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;

KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac;

KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.

OS Homo sapiens.

PN WO200158956-A2.

PD 16-AUG-2001.

PF 09-FEB-2001; 2001WO-US04170.

PR 10-FEB-2000; 2000US-0181608.

PA (BAD1) BASF AG.

PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;

PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;

PI Leonard SN;

DR WPI; 2001-550020/61.

PT Novel antibodies and compounds capable of binding to human

PT interleukin-18 useful for treating, e.g., inflammatory disorders,

PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

PS Examples; Page 79-80; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody LT28
CC comprising the heavy chain and light chain sequences joined by a linker.

XX Sequence 235 AA;

Query Match 100.0%; Score 580; DB 22; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,7e-38;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSVLTQPPSASGTPGQRTISCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDRPSGYP 60

Db 125 QSVLTQPPSASGTPGQRTISCGSSSSNIGINAVMYQQLPGTAPKLLIYGNDRPSGYP 184

QY 61 DRFGSGSGTSASLAIISGLQSEDEADYCCAMPDLSGPFVGGGKTLTVLG 111

Db 185 DRFGSGSGTSASLAIISGLQSEDEADYCCAMPDLSGPFVGGGKTLTVLG 235

RESULT 3

AA655355 standard; protein; 111 AA.

AC AA655355;

DT 30-NOV-2001 (first entry)

DE Anti-IL-18 antibody LT28 light chain sequence.

XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;

KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac;

KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.

OS Homo sapiens.

PN WO200158956-A2.

PD 16-AUG-2001.

PF 09-FEB-2001; 2001WO-US04170.

PR 10-FEB-2000; 2000US-0181608.

PA (BAD1) BASF AG.

PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;

PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;

PI Leonard SN;

DR WPI; 2001-550020/61.

DR N-PSDB; AAH47514.

PT Novel antibodies and compounds capable of binding to human

PT interleukin-18 useful for treating, e.g., inflammatory disorders,

PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

PS Example 2; Page 90; 91pp: English.

CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody LT28
CC light chain sequence.

SO Sequence 111 AA:

Query Match 97.6%; Score 566; DB 22; Length 111;
Best Local Similarity 98.2%; Pred. No. 1.6e-37;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QSVLTQPPASGTPGQRYTISCGSSSSNIGINAVNMVYQQLPRTAKRLIYGNDRPSGVP 60

DB 1 QSVLTQPPASGTPGQRYTISCGSSSSNIGINAVNMVYQQLPRTAKRLIYGNDRPSGVP 60

OY 61 DRPSGSGTSSAISIAGLQSEDEADYCAAMDLSLGPVFGGKTLTVLG 111

DB 61 drfsgsksgtsasalslsglqseadeadycaawddslrsivfvggkltlvlg 111

RESULT 4

AAB46058 ID AAB46058 standard; Peptide; 240 AA.

AC AAB46058;

DT 23-MAR-2001 (first entry)

DE Human TF anti-idiotypic antibody fragment Z4A.

KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;
KW anti-idiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;
KW antiparasitic; infectious disease.

OS Homo sapiens.

PN WO200073430-A2.

PD 07-DEC-2000.

PF 29-MAY-2000; 2000WO-DE01809.

PR 27-MAY-1999; 99DE-1024405.

PR 09-SEP-1999; 99DE-1043016.

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

PI Goletz S, Karsten U;

DR WPI: 2001-049937/06.

XX Vaccines against conformation-dependent or non-peptide antigens, based
PT on DNA encoding peptide which mimics the antigen, useful e.g. as
PT antitumor vaccines -
XX

PS Disclosure; Page 13; 36pp: German.

CC This invention describes a novel vaccine (V1) against
CC conformation-dependent antigens (CDA) comprising DNA (I) and/or an
CC antibody, or peptide which immunologically imitates CDA, is new. (I)
CC encodes a region of an anti-idiotypic antibody (Ab2) or another peptide
CC which: (a) specifically binds to the binding site of an antibody (Ab1)
CC or an antigen binding molecule; and (b) immunologically mimics the
CC initial antigen. The epitope is partially or completely
CC conformation-dependent, and has an immunogenic structure defined by a
CC specific spatial conformation of amino acids. (I) is used in the form
CC of linear or circular naked DNA and/or with a viral vector and/or
CC adjuvants. The products of the invention have cytostatic, virucidal,
CC antibacterial and antiparasitic. The invention also describes (1) a
CC corresponding vaccine (V2) against antigens which are not proteins or
CC peptides, as defined above but which have epitopes which show an
CC immunogenic structure; (2) preparing (V1) and (V2); (3) human
CC anti-idiotypic antibody fragments against the MUC1-conformation epitope
CC having one of 31 approximately 60 residue amino acid sequences, all
CC fully defined in the specification; (4) MUC1-conformation epitope mimics
CC having one of 16 9-17 residue amino acid sequences, all fully in the
CC specification; (5) anti-idiotypic antibody fragments against the TF
CC antigen having one of 24 approximately 200 residue amino acid sequences,
CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
CC having one of 25 7-13 residue amino acid sequences, all fully defined in
CC the specification; and (7) DNA sequences encoding the fragments and
CC derivatives defined in (3), (4), (5), or (6). (V1) and (V2) are used to treat
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
CC and parasites. The vaccines are effective in cases where vaccination has
CC previously not been possible.

SO Sequence 240 AA:

Query Match 92.8%; Score 538; DB 22; Length 240;
Best Local Similarity 93.7%; Pred. No. 5.5e-35;
Matches 104; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 QSVLTQPPASGTPGQRYTISCGSSSSNIGINAVNMVYQQLPRTAKRLIYGNDRPSGVP 60

DB 130 QSVLTQPPASGTPGQRYTISCGSSSSNIGINAVNMVYQQLPRTAKRLIYGNDRPSGVP 189

OY 61 DRPSGSGTSSAISIAGLQSEDEADYCAAMDLSLGPVFGGKTLTVLG 111

DB 190 drfsgsksgtsasalslsglqseadeadycaawddslrsivfvggkltlvlg 240

RESULT 5

AAB46060 ID AAB46060 standard; Peptide; 244 AA.

AC AAB46060;

DT 23-MAR-2001 (first entry)

DE Human TF anti-idiotypic antibody fragment Z4A.

KW MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;
KW anti-idiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;
KW antiparasitic; infectious disease.

OS Homo sapiens.

PN WO200073430-A2.

PD 07-DEC-2000.

PF 29-MAY-2000; 2000WO-DE01809.

PR 27-MAY-1999; 99DE-1024405.

PR 09-SEP-1999; 99DE-1043016.

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX
PI Goletz S, Karsten U;
XX
DR WPI; 2001-049937/06.
XX
PT Vaccines against conformation-dependent or non-peptide antigens, based
PT on DNA encoding peptide which mimics the antigen, useful e.g. as
PT antitumor vaccines -
XX
PS Disclosure; Page 14; 36pp; German.
XX
CC This invention describes a novel vaccine (V1) against
CC conformation-dependent antigens (CDA) comprising DNA (I) and/or an
CC antibody, or peptide which immunologically imitates CDA, is new. (I)
CC encodes a region of an anti-idiotypic antibody (Ab2) or another peptide
CC which: (a) specifically binds to the binding site of an antibody (Ab1)
CC or an antigen binding molecule; and (b) immunologically mimics the
CC initial antigen. The epitope is partially or completely
CC conformation-dependent, and has an immunogenic structure defined by a
CC specific spatial conformation of amino acids. (I) is used in the form
CC of linear or circular naked DNA and/or with a viral vector and/or
CC adjuvants. The products of the invention have cytostatic, virucidal,
CC antibacterial and antiparasitic. The invention also describes (1) a
CC corresponding vaccine (V2) against antigens which are not proteins or
CC peptides, as defined above but which have epitopes which show an
CC immunogenic structure; (2) preparing (V1) and (V2); (3) human
CC anti-idiotypic antibody fragments against the MUC1-conformation epitope
CC having one of 31 approximately 60 residue amino acid sequences, all
CC fully defined in the specification; (4) MUC1-conformation epitope mimics
CC having one of 16 9-17 residue amino acid sequences, all fully in the
CC specification; (5) anti-idiotypic antibody fragments against the TF
CC antigen having one of 24 approximately 200 residue amino acid sequences,
CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
CC having one of 25 7-13 residue amino acid sequences, all fully defined in
CC the specification; and (7) DNA sequences encoding the fragments and
CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
CC and parasites. The vaccines are effective in cases where vaccination has
CC previously not been possible.
XX
SQ Sequence 244 AA:
XX
Query Match 92.8%; Score 538; DB 22; Length 244;
Best Local Similarity 93.7%; Pred. No. 5.6e-35;
Matches 104; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 OSVLTOPPSSAGTGGORVTRISGSSSSNIGINAWMYOOLPCTARKLLTYGNDORSGVP 60
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
134 qsvltqppssagtpgqrvtliscgsssnvsnltwmyqdlpgtapklltysmngpssgvp 193
QY 61 DRFSGSKSGTSASLAISGLQSEDEADYYCAAWMDLSLGPFGGCTRLTVLG 111
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
194 drfsgsksgtsaslaissglqsedeadyycaawmdslrslvfygggkltvlvg 244
XX
RESULT 6
AAB46061
ID AAB46061 standard; Peptide; 241 AA.
XX
AC AAB46061;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human TF anti-idiotypic antibody fragment 29.
XX
KW MUC1: human; vaccine: conformation-dependent antigen; antibody; cancer;
KW anti-idiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;
KW antiparasitic; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200073430-A2.

XX
PD 07-DEC-2000.
XX
XX
PF 29-MAY-2000; 2000WO-DE01809.
XX
XX
PR 27-MAY-1999; 99DE-1024405.
PR 09-SEP-1999; 99DE-1043016.
XX
XX
PA (DELB-) DELBROECK CENT MOLEKULARE MEDIZIN MAX.
XX
XX
PI Goletz S, Karsten U;
XX
DR WPI; 2001-049937/06.
XX
PT Vaccines against conformation-dependent or non-peptide antigens, based
PT on DNA encoding peptide which mimics the antigen, useful e.g. as
PT antitumor vaccines -
XX
PS Disclosure; Page 14; 36pp; German.
XX
CC This invention describes a novel vaccine (V1) against
CC conformation-dependent antigens (CDA) comprising DNA (I) and/or an
CC antibody, or peptide which immunologically imitates CDA, is new. (I)
CC encodes a region of an anti-idiotypic antibody (Ab2) or another peptide
CC which: (a) specifically binds to the binding site of an antibody (Ab1)
CC or an antigen binding molecule; and (b) immunologically mimics the
CC initial antigen. The epitope is partially or completely
CC conformation-dependent, and has an immunogenic structure defined by a
CC specific spatial conformation of amino acids. (I) is used in the form
CC of linear or circular naked DNA and/or with a viral vector and/or
CC adjuvants. The products of the invention have cytostatic, virucidal,
CC antibacterial and antiparasitic. The invention also describes (1) a
CC corresponding vaccine (V2) against antigens which are not proteins or
CC peptides, as defined above but which have epitopes which show an
CC immunogenic structure; (2) preparing (V1) and (V2); (3) human
CC anti-idiotypic antibody fragments against the MUC1-conformation epitope
CC having one of 31 approximately 60 residue amino acid sequences, all
CC fully defined in the specification; (4) MUC1-conformation epitope mimics
CC having one of 16 9-17 residue amino acid sequences, all fully in the
CC specification; (5) anti-idiotypic antibody fragments against the TF
CC antigen having one of 24 approximately 200 residue amino acid sequences,
CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
CC having one of 25 7-13 residue amino acid sequences, all fully defined in
CC the specification; and (7) DNA sequences encoding the fragments and
CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
CC and parasites. The vaccines are effective in cases where vaccination has
CC previously not been possible.
XX
SQ Sequence 241 AA:
XX
Query Match 92.6%; Score 537; DB 22; Length 241;
Best Local Similarity 92.8%; Pred. No. 6.6e-35;
Matches 103; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 OSVLTOPPSSAGTGGORVTRISGSSSSNIGINAWMYOOLPCTARKLLTYGNDORSGVP 60
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
131 qsvltqppssagtpgqrvtliscgsssnvsnltwmyqdlpgtapklltysmngpssgvp 190
QY 61 DRFSGSKSGTSASLAISGLQSEDEADYYCAAWMDLSLGPFGGCTRLTVLG 111
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
191 drfsgsksgtsaslaissglqsedeadyycaawmdslrslvfygggkltvlvg 241
XX
RESULT 7
AAG65555
ID AAG65555 standard; protein; 118 AA.
XX
AC AAG65555;
XX
DT 30-NOV-2001 (first entry)
XX

DE Amino acid sequence of protein seq Id No. 80.
 XX Gene library; Immunoglobulin; antibody library; human.
 XX Homo sapiens.
 OS
 XX WO200162907-A1.
 PN
 XX 30-AUG-2001.
 PD
 XX 22-FEB-2001; 2001WO-JP01298.
 PF
 XX 22-FEB-2000; 2000JP-0050543.
 PR
 XX (MED-) MEDICAL & BIOLOGICAL LAB CO LTD.
 PA
 XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
 PI Okuno Y, Shitaki K;
 XX WPI; 2001-565420/63.
 DR N-PSDB; AAA47719.
 DR
 XX
 PT Producing gene libraries and antibody libraries, involves selecting a
 PT light chain that binds to a heavy chain product to produce a functional
 PT formation, and producing a gene library of the light chain variable
 PT regions -
 PS Examples; p 152-153; 181pp; Japanese.
 XX
 CC The invention relates to producing gene libraries, comprising
 CC immunoglobulin light and heavy variable region. The method involves
 CC selecting light chain that binds with the heavy chain product to produce
 CC a functional conformation, producing a gene library comprising a
 CC collection of these light chain variable genes, and combining with gene
 CC library of heavy chain variable genes. The method is used for production
 CC of gene and antibody libraries.
 CC
 XX
 SQ Sequence 118 AA;
 Query Match 92.5%; Score 536.5; DB 22; Length 118;
 Best Local Similarity 93.8%; Pred. No. 3.5e-35;
 Matches 103; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMYQQLPGTAPKLLIYGNDRPSGVP 60
 DB 1 qsvltqppsaagtpgqrvltiscgsssnigtvnmwyqlpgtapklllysnqrpssgvp 60
 QY 61 DRFGSGKSGTASLAISGLQSEDEADYICAMWDSLSG-PVFGGKTLTVLG 111
 DB 61 drfsgsksgtsaslaaisglqseadeadyicaawdslingyvvf99gkltvlg 112
 RESULT 8
 ID AAR8506 standard; Protein; 111 AA.
 AC AAR8506;
 XX
 DT 31-JUN-1996 (first entry)
 DE VLambda for antibody BT34/A5.
 XX
 KW Antibody; variable light chain; VLambda; human; monoclonal; BT34/A5;
 KW BT32/A6; cell cycle independent; tumour specific; glioma; therapy; Mab;
 KW detection; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 23..35
 FT /note= "complementarity determining region (specifically
 FT claimed)"

FT Region 51..57
 FT /note= "complementarity determining region (specifically
 FT claimed)"
 FT Region 90..100
 FT /note= "complementarity determining region (specifically
 FT claimed)"
 PN WO9535374-A1.
 XX
 PD 28-DEC-1995.
 PF 16-JUN-1995; 95WO-CA00361.
 PR 21-JUN-1994; 94US-0264093.
 PA (DANW/) DAN M D.
 PI Dan MD;
 XX WPI; 1996-058411/06.
 DR N-PSDB; AAT10940.
 DR
 XX
 PT Novel monoclonal antibodies, BT34/A5 and BT32/A6 - used to
 PT characterise glioma specific cell surface antigens, and in the
 PT treatment of glioma
 PS Claim 11; Page 34; 53pp; English.
 XX
 CC AAR8504-R88510 represent regions of the human monoclonal antibodies
 CC (Mab's) BT34/A5 and BT32/A6. This sequence represents the variable
 CC region of the light chain, subgroup lambda, (VLambda) of BT34/A5. The
 CC complementarity determining regions (CDR's) of this sequence are
 CC specifically claimed. This sequence preferably has an N-terminal
 CC extension comprising the signal sequence represented by AAR8507. The
 CC BT34/A5 and BT32/A6 Mab's recognise a cell cycle independent tumour
 CC specific antigen. They also bind equally well to tumour cells in vitro
 CC regardless of their culture viability, growth characteristics, or
 CC culture density. The antibodies effectively label the tumour cells by
 CC binding to the antigen present on the cell surface. The Mab's are useful
 CC in the detection and the treatment of glioma. These Mab's are specific
 CC for glioma and show none of the cross-reactivity seen with previous
 CC antibodies.
 CC
 XX
 SQ Sequence 111 AA;
 Query Match 91.9%; Score 533; DB 17; Length 111;
 Best Local Similarity 91.9%; Pred. No. 6.3e-35;
 Matches 102; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMYQQLPGTAPKLLIYGNDRPSGVP 60
 DB 1 qsvltqppsaagtpgqrvltiscgsssnigtvnmwyqlpgtapklllysnqrpssgvp 60
 QY 61 DRFGSGKSGTASLAISGLQSEDEADYICAMWDSLSG-PVFGGKTLTVLG 111
 DB 61 drfsgsksgtsaslaaisglqseadeadyicaawdsikyvfv99gkltvlg 111
 RESULT 9
 ID AAW90281 standard; Protein; 111 AA.
 AC AAW90281;
 XX
 DT 07-SEP-1999 (first entry)
 DE Human anti-GPIIb/IIIa antibody light chain protein from phagemid pG13.
 XX
 KW Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
 KW blood platelet membrane protein; predisposition; prevention; treatment;
 KW autoimmune thrombocytopenic purpura; AITP; fibrinogen binding; thrombi;
 KW thrombocyte; cardiac infarction; pulmonary embolism; light chain.


```

QY      61 DREFGSGSGTSASLAISLQSEDEADYYCAAWDLSLGPYFEGGGTKLFLVLC 111
      |||
      80 drfsgsgtsaslaaislqsedeadyycaawdslngwfggktkltlvg 130
      |||

```

RESULT 13
AAG62955
ID AAG62955 standard; Protein; 111 AA

DT 01-OCT-2001 (first entry)

DE Amino acid sequence of variable light chain fragment of clone G92.
XX
Antibody; light chain; V_H; amyloid protein; blood brain barrier;
endothelial cell; brain cell antigen; inflammation; adhesion molecule;
transferrin receptor; neurological disease; Alzheimer's disease;
prion disease; AIDS-related dementia; epilepsy; brain injury.

PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases -

The present sequence represents an antibody variable light chain (VL) fragment. The fragment is used to produce a mixture or panel of 5 different specific binding members, each comprising an antibody VH and/or VL variable domain and capable, when displayed on the surface of filamentous bacteriophage particles or in the case of a specific binding member comprising the D5 VH and/or VL variable domain when bound to human serum amyloid protein, to pass through a mammalian blood brain barrier (BBB). The panel is useful for the selection of specific binding members with a desired property such as ability to cross BBB, ability to bind endothelial cells or other brain cell antigen ability to bind areas of inflammation in the brain or BBB breakdown or ability to bind intracellular adhesion molecules and to bind transferrin receptor. The antibodies are useful in diagnosis, prophylaxis and treatment of human or animal body, including neurological diseases, such as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy and traumatic brain injury and any diseases involving inflammation occurring within the brain or central nervous system.

Query Match	90.9%;	Score 527;	DB 22;	Length 111;
Best Local Similarity	89.2%;	Pred. No. 1.9e-34;		
Matches	99;	Conservative	5;	Mismatches 7;
			Indels	0;
			Gaps	0

```
QY      61 DRFGSGKSGTSASLAISGLQSEDEADYYICAMWDSLSGPVREGGTKTLVLG 111111
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 drfsgsgtsqslvislqsdeadyycaswdslngrvifgsgtkltvlg 111111
```

RESULT	14
AAV21881	
ID	AAV21881 standard; Protein; 242 AA
XX	
AC	AAV21881;

DE Amino acid sequence of antibody ITA3.

KW Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody;
KW diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy
KW ITA3.

PN	EP934953-A2.	
XX		
PD	11-AUG-1999.	
XX		
PF	01-DEC-1998;	98EP-0122546
XX		
PR	03-DEC-1997;	97US-0067428

PT New anti-complex antibody useful for diagnosing prostate cancer
XX
PS Claim 26; Page 20-21; 42pp; English.

Query Match	90.98;	Score 527;	DB 20;	Length 242;
Best Local Similarity	92.88;	Pred. No. 4.1e-34;		
Matches 103; Conservative	2;	Mismatches 6;	Indels 0;	Gaps 0;

QY 61 DRFGSKGTSASLAISGLQSEDEADYYCAAWDDSLSGPVFGGKTLVLG 111

Db 192 drfsgskstsaiaisglrseadadycaawodsaisalvfggkltlvig 242

RESULT 15
AAV21883
ID AAV21883 standard; Protein; 244 AA.
XX
AC AAV21883;
XX
DT 24-SEP-1999 (first entry)
XX

DE Amino acid sequence of antibody BIOA8.

KM Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody;
KW diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy;
KW BIOA8.

XX Homo sapiens.

XX
FH Key Location/Qualifiers
FT Misc-difference 201
FT /label= "unknown"
FT /note= "encoded by TSP"

PN EP934953-A2.

XX 11-AUG-1999.

PF 01-DEC-1998; 98EP-0122546.

PR 03-DEC-1997; 97US-0067428.

XX (BOE) BOEHRINGER MANNHEIM CORP.

PI Mahoney W, Sawyer JR, Winter GP;

XX WPI; 1999-432068/37.

DR N-PSDB; AAX86940.

XX New anti-complex antibody useful for diagnosing prostate cancer

PS Claim 28; Page 25-27; 42pp; English.

XX
XX The invention relates to an antibody that binds a complex between
CC prostate-specific antigen (PSA) and anti-chymotrypsin (ACT), and has an
CC affinity for the complex which is at least 10 fold higher than the
CC affinity for either PSA or ACT alone. The antibody is used in diagnostic
CC assays to detect PSA-ACT in serum samples from patients. The levels of
CC PSA-ACT complex increase in patients suffering from prostate cancer
CC compared to the levels in patients with benign or no growths in the
CC prostate. Therefore detection of PSA in complex with ACT is useful for
CC the early detection of prostate tumours, by distinguishing between
CC benign and malignant conditions of the prostate as well as for the
CC management of patients with prostate cancer, such as the disclosure of
CC metastasis and the monitoring of the PSA levels after treatment. The
CC antibodies may also be used in immunotherapy, affinity chromatography
CC and isolation or purification of PSA-ACT. Unlike prior art antibodies
CC which bind to PSA-ACT complexes but may also bind PSA or ACT alone, the
CC present antibody is specific for PSA-ACT alone. Diagnostic assays using
CC the antibodies are more accurate in diagnosing prostate cancer as they
CC only detect the intact complex of PSA-ACT. Sequences AAV21880-884
CC represent specific examples of antibodies directed against PSA-ACT. The
CC present sequence represents the amino acid sequence of antibody BIOA8.
XX
XX

SQ Sequence 244 AA;

Query Match 90.3%; Score 524; DB 20; Length 244;

Best Local Similarity 91.9%; Pred. No. 7e-34;

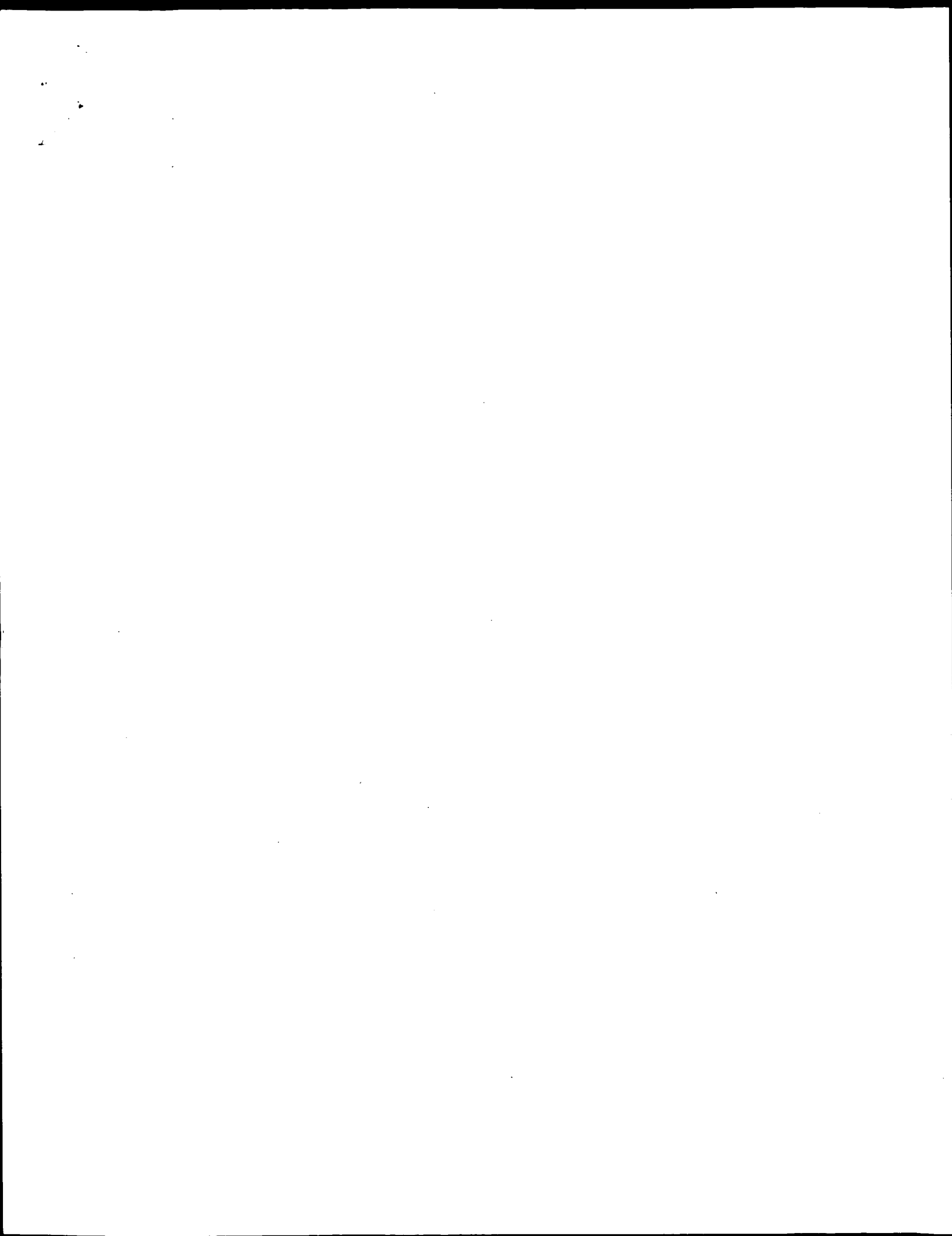
Matches 102; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 QSVLTQPPSASGTSGVTSISGSSSSNIGINAVMWYQQLPTAPKLLIYGNDRPSGVP 60

Db 134 qsvltqppsaqtlpqrvtlscsgssnlgsmwyvqqldptapklllyrnmqrpqvp 193

OY 61 DRFSGSKSGTSASIALISGLQSEDEADYCAAMDLSLGPVFGGKLTVLG 111
DB 194 drfsgskxqtsasiaslsglrseadadycaawodsirgivrfggkltlvig 244

Search completed: June 21, 2002, 09:20:17
Job time: 430 sec



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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:43 ; Search time 109.39 Seconds

(without alignments)
97.504 Million cell updates/sec

Title: US-09-780-035-29

Perfect score: 580

Sequence: 1 OSVLTPPSASGTPGQRYVTL.....WDSLSGPFVGGGKTLVLG 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR-71:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	545	94.0	233	2	S25752	Ig lambda chain -
2	533	91.9	235	2	S25750	Ig lambda chain -
3	532	91.7	129	2	S78058	Ig lambda chain pr
4	527	90.9	112	2	B44151	Ig lambda chain V
5	526	90.7	112	2	D44151	Ig lambda chain V
6	526	90.7	234	2	S25757	Ig lambda chain V
7	524	90.3	112	2	C44151	Ig lambda chain V
8	523	90.3	149	2	S23626	Ig lambda chain V
9	523	90.2	130	2	S78057	Ig lambda chain pr
10	522	90.0	216	2	A42193	Ig lambda chain (B
11	514	88.6	110	2	S57408	Ig lambda chain V-
12	513	88.4	112	2	A44151	Ig lambda chain V
13	506.5	87.3	235	2	S25754	Ig lambda chain -
14	505	87.1	233	2	S25744	Ig lambda chain -
15	504	86.9	110	2	S57428	Ig light chain V-J
16	496	85.5	111	1	L1H0V0	Ig lambda chain V-
17	488	84.1	98	2	S36047	Ig lambda chain -
18	488	84.1	117	2	S23627	Ig lambda chain pr
19	479.5	82.7	112	1	L1H0M1	Ig lambda chain V-
20	478	82.4	216	2	S03401	Ig lambda chain (K
21	478	82.4	235	2	S05270	Ig lambda chain pr
22	477	82.2	109	1	S47009	Ig lambda chain V1
23	476	82.1	109	1	L1H0W4	Ig lambda chain V-
24	475	81.9	98	2	S36048	Ig lambda chain -
25	470.5	81.1	112	2	S51148	Ig lambda chain -
26	470	81.0	130	1	L1H0B1	Ig lambda chain pr
27	469	80.9	130	2	S09712	Ig lambda chain V
28	464	80.0	111	1	L1H0G1	Ig lambda chain V-
29	463.5	79.9	112	1	L1H0H4	Ig lambda chain V-

30	462	79.7	111	2	S36274	Ig lambda chain V
31	460	79.3	216	2	S29258	Ig lambda chain V
32	458.5	79.1	213	2	S21066	Ig lambda chain V
33	458	79.0	131	2	S24321	Ig lambda chain pr
34	457	78.8	232	2	S25742	Ig lambda chain V
35	456	78.6	113	2	A23700	Ig lambda chain V
36	452	77.9	110	2	S36258	Ig lambda chain V
37	451.5	77.8	236	2	S25746	Ig lambda chain -
38	451	77.4	111	2	S19664	Ig lambda chain V
39	449	77.4	111	2	S47185	Ig lambda chain V
40	449	76.0	145	2	S25743	Ig lambda chain -
41	437	75.3	111	1	L1H0W1	Ig lambda chain V-
42	435	75.0	98	2	S36046	Ig lambda chain V-
43	434	74.8	109	1	L1H0E1	Ig lambda chain V-
44	433.5	74.7	217	2	JE0246	Ig lambda chain NI
45	432.5	74.6	99	2	S36054	Ig lambda chain -

ALIGNMENTS

RESULT 1
S25752
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25752
R:Combiarto, G.; Kiobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162
A:Accession: S25752
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57817; NID:q33733; PIND:CAA40954.1; PID:q33734
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 545; DB 2; Length 233;
Best Local Similarity 94.6%; Pred. No. 3.1e-39;
Matches 105; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 OSVLTPPSASGTPGQRYVTLSCGSSSSNIGINAVMYQDLPETAPKLLIYNDQRPSPGP 60
DB 18 OSVLTPPSASGTPGQRYVTLSCGSSSSNIGSNVWYQDLPETAPKLLIYRNQRPSPGP 77
QY 61 DRFGSKSGTSASLAISGLQSEDEADYCAAMDLSGPFVGGGKTLVLG 111
DB 78 DRFGSKSGTSASLAISGLQSEDEADYCAAMDLSGPFVGGGKTLVLG 128

RESULT 2
S25750
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25750
R:Combiarto, G.; Kiobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162
A:Accession: S25750
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57815; NID:q33729; PIND:CAA40952.1; PID:q33730
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 91.9%; Score 533; DB 2; Length 235;
Best Local Similarity 92.8%; Pred. No. 3.2e-38;
Matches 103; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMVYQQLPGTAPKLLIYGNDQRPSSGVP 60
|||||
DB 20 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMVYQQLPGTAPKLLIYRNQRPSSGVP 79
|||||

OY 61 DRFSGSGKGTASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLYVLG 111
|||||
DB 80 DRFSGSGKGTASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLYVLG 130
|||||

RESULT 3
S78058
Ig lambda chain precursor V-J region (clone mAb 67VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78058; S23723
R:Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78058
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262
A:Accession: S23723
A:Molecule type: mRNA
A:Residues: 19-129 <HAR>
A:Cross-references: EMBL:X54446
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-18/Domain: signal sequence (fragment) #status predicted <sig>
F:19-129/Product: Ig lambda chain (fragment) #status predicted <mat>
F:33-109/Domain: immunoglobulin homology <imm>

Query Match 91.7%; Score 532; DB 2; Length 129;
Best Local Similarity 93.7%; Pred. No. 2.1e-38;
Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMVYQQLPGTAPKLLIYGNDQRPSSGVP 60
|||||
DB 19 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMVYQQLPGTAPKLLIYRNQRPSSGVP 78
|||||

OY 61 DRFSGSGKGTASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLYVLG 111
|||||
DB 79 DRFSGSGKGTASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLYVLG 129
|||||

RESULT 4
B44151
Ig lambda chain V region (BO-09) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: B44151
R:Zedede, S.L.; Barbash III, C.F.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.; Pya
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746
A:Accession: B44151
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-112 <ZEB>
A:Cross-references: GB:M88310; NID:g183954; PIDN:AAA5968.1; PID:g183955
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

F:14-90/Domain: immunoglobulin homology <imm>

Query Match 90.9%; Score 527; DB 2; Length 112;
Best Local Similarity 91.7%; Pred. No. 4.8e-38;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 4 LTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMVYQQLPGTAPKLLIYGNDQRPSSGVPDRF 63
|||||
DB 3 LTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMVYQQLPGTAPKLLIYNNRPSGVPDRF 62
|||||

OY 64 SSKSGKGTASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLYVLG 111
|||||
DB 63 SSKSGKGTASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLYVLG 110
|||||

RESULT 5
D44151
Ig lambda chain V region (BO-12) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: D44151
R:Zedede, S.L.; Barbash III, C.F.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.;
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746
A:Accession: D44151
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-112 <ZEB>
A:Note: nucleotide translation is not given
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-90/Domain: immunoglobulin homology <imm>

Query Match 90.7%; Score 526; DB 2; Length 112;
Best Local Similarity 93.5%; Pred. No. 5.9e-38;
Matches 100; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 LTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMVYQQLPGTAPKLLIYGNDQRPSSGVPDRF 63
|||||
DB 3 LTQPPSASGTPGQRTVITSCGSSSSNIGINAVNMVYQQLPGTAPKLLIYNNRPSGVPDRF 62
|||||

OY 64 SSKSGKGTASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLYVLG 110
|||||
DB 63 SSKSGKGTASLAISGLQSEDEADYYCAAMDLSLGPVFGGKTLYVLG 109
|||||

RESULT 6
S25757
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25757
R:Combrilato, G.; Klobock, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and V(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162
A:Accession: S25757
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-234 <COM>
A:Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:149-217/Domain: immunoglobulin homology <imm>

Query Match 90.7%; Score 526; DB 2; Length 234;
Best Local Similarity 89.2%; Pred. No. 1.3e-37;
Matches 99; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:48:18 ; Search time 52.75 Seconds

(without alignments)
81.476 Million cell updates/sec

Title: US-09-780-035-29

Perfect score: 580

Sequence: 1 QSVLTQPPASGTPGQRTVLT.....WDSLSPGPFEGGTRKLTVLG 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	496	85.5	111	LV1A_HUMAN	P01699 homo sapien
2	479.5	82.7	112	LV1H_HUMAN	P06887 homo sapien
3	476	82.1	109	LV1F_HUMAN	P04208 homo sapien
4	470	81.0	130	LV1C_HUMAN	P06316 homo sapien
5	464	80.0	111	LV1D_HUMAN	P01702 homo sapien
6	463.5	79.9	112	LV1B_HUMAN	P01700 homo sapien
7	437	75.3	111	LV1C_HUMAN	P01701 homo sapien
8	434	74.8	109	LV1I_HUMAN	P06888 homo sapien
9	389	67.1	111	LV2G_HUMAN	P01710 homo sapien
10	385	66.4	111	LV2I_HUMAN	P01712 homo sapien
11	383	66.0	103	LV1E_HUMAN	P01703 homo sapien
12	378.5	65.3	112	LV2K_HUMAN	P04209 homo sapien
13	377	65.0	111	LV2F_HUMAN	P01709 homo sapien
14	375	64.7	111	LV2D_HUMAN	P01707 homo sapien
15	374	64.5	111	LV2C_HUMAN	P01706 homo sapien
16	367.5	63.4	110	LV2J_HUMAN	P01713 homo sapien
17	365	62.9	109	LV2E_HUMAN	P01708 homo sapien
18	364	62.8	111	LV2B_HUMAN	P01705 homo sapien
19	358	61.7	111	LV2H_HUMAN	P01711 homo sapien
20	344	59.3	106	LV4E_HUMAN	P06889 homo sapien
21	339	58.4	111	LV6D_HUMAN	P06318 homo sapien
22	338.5	58.4	131	LV6E_HUMAN	P06319 homo sapien
23	337	58.1	106	LV4A_HUMAN	P01715 homo sapien
24	334	57.6	107	LV4C_HUMAN	P01717 homo sapien
25	333	57.4	108	LV5A_HUMAN	P01719 homo sapien
26	332.5	57.3	112	LV6A_HUMAN	P01721 homo sapien
27	331	57.1	111	LV3B_HUMAN	P08078 homo sapien
28	330	56.9	111	LV2A_HUMAN	P01704 homo sapien
29	325	56.0	106	LV4B_HUMAN	P01716 homo sapien
30	320	55.2	108	LV3A_HUMAN	P01718 homo sapien
31	320	55.0	111	LV2L_HUMAN	P06422 homo sapien
32	319	55.0	111	LV6C_HUMAN	P06317 homo sapien
33	313	54.0	106	LV4D_HUMAN	P01718 homo sapien

ALIGNMENTS

RESULT	ID	Query Match	Score	DB ID	Description
1	LV1A_HUMAN	85.5%	496	111 AA	P01699
2	LV1H_HUMAN	82.7%	479.5	112 AA	P06887
3	LV1F_HUMAN	82.1%	476	109 AA	P04208
4	LV1C_HUMAN	81.0%	470	130 AA	P06316
5	LV1D_HUMAN	80.0%	464	111 AA	P01702
6	LV1B_HUMAN	79.9%	463.5	112 AA	P01700
7	LV1C_HUMAN	75.3%	437	111 AA	P01701
8	LV1I_HUMAN	74.8%	434	109 AA	P06888
9	LV2G_HUMAN	67.1%	389	111 AA	P01710
10	LV2I_HUMAN	66.4%	385	111 AA	P01712
11	LV1E_HUMAN	66.0%	383	103 AA	P01703
12	LV2K_HUMAN	65.3%	378.5	112 AA	P04209
13	LV2F_HUMAN	65.0%	377	111 AA	P01709
14	LV2D_HUMAN	64.7%	375	111 AA	P01707
15	LV2C_HUMAN	64.5%	374	111 AA	P01706
16	LV2J_HUMAN	63.4%	367.5	110 AA	P01713
17	LV2E_HUMAN	62.9%	365	109 AA	P01708
18	LV2B_HUMAN	62.8%	364	111 AA	P01705
19	LV2H_HUMAN	61.7%	358	111 AA	P01711
20	LV4E_HUMAN	59.3%	344	106 AA	P06889
21	LV6D_HUMAN	58.4%	339	111 AA	P06318
22	LV6E_HUMAN	58.4%	338.5	131 AA	P06319
23	LV4A_HUMAN	58.1%	337	106 AA	P01715
24	LV4C_HUMAN	57.6%	334	107 AA	P01717
25	LV5A_HUMAN	57.4%	333	108 AA	P01719
26	LV6A_HUMAN	57.3%	332.5	112 AA	P01721
27	LV3B_HUMAN	57.1%	331	111 AA	P08078
28	LV2A_HUMAN	56.9%	330	111 AA	P01704
29	LV4B_HUMAN	56.0%	325	106 AA	P01716
30	LV3A_HUMAN	55.2%	320	108 AA	P01718
31	LV2L_HUMAN	55.0%	320	111 AA	P06422
32	LV6C_HUMAN	55.0%	319	111 AA	P06317
33	LV4D_HUMAN	54.0%	313	106 AA	P01718

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RA MEDLINE=85257662; PubMed=2410269;
 RA Mhaesco E., Roy J.P., Congy N., Pernat-Rivat L., Mhaesco C.;
 RT "The amino acid sequence of a lambda light chain presenting abnormal
 RT physicochemical and antigenic features."
 RL Eur. J. Biochem. 150:349-357(1985).
 CC -1- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
 CC WERE POSITIONED BY HOMOLOG.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
 CC MARKERS.
 CC PIR: A25479; LIHUM.
 DR HSSP: P01703; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region; Monoclonal antibody.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 90 BY SIMILARITY.
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 11789 MW; 74812AF079CFFBE4 CRC64;

Query Match 82.7%; Score 479.5; DB 1; Length 112;
 Best Local Similarity 85.6%; Pred. No. 1,3e-37;
 Matches 95; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGIN-ANVMYQQLPGLTAPKLLIYGNDRPSGVP 59
 DB 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGIN-ANVMYQQLPGLTAPKLLIYVNGRPSGV 60
 QY 60 PDFFSSKSGTASLAISGLQSEDEADYICAMDSLSGPVGGGKTLTVL 110
 DB 61 PDFFSSKSGTASLAISGLQSEDEADYICAMDSLSGTVGGTGTATV 111

RESULT 3
 LVIF_HUMAN
 ID LVIF_HUMAN STANDARD; PRT; 109 AA.
 AC P04208;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-I region WAH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=83221661; PubMed=6407018;
 RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
 RT "Complete covalent structure of a human immunoglobulin D: sequence of
 RT the lambda light chain."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
 DR PIR: A01967; LIHWA.
 DR HSSP: P01703; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 97 V SEGMENT.
 FT DOMAIN 98 109 J SEGMENT.
 FT DISULFID 22 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 82.1%; Score 476; DB 1; Length 109;
 Best Local Similarity 87.3%; Pred. No. 2,7e-37;
 Matches 96; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGIN-ANVMYQQLPGLTAPKLLIYGNDRPSGVP 60
 DB 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGIRYVYVYQQLPGLTAPKLLIYKDNDRPSGVP 60
 QY 61 DFFSSKSGTASLAISGLQSEDEADYICAMDSLSGPVGGGKTLTVL 110
 DB 61 DFFSSKSGTASLAISGLQSEDEADYICAMDSLSL-VGGGTTTLTVL 108

RESULT 4
 LVIG_HUMAN
 ID LVIG_HUMAN STANDARD; PRT; 130 AA.
 AC P06316;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-I region BL2 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85062823; PubMed=6095199;
 RA Tsujimoto Y., Croce C.M.;
 RT "Molecular cloning of a human immunoglobulin lambda chain variable
 RT sequence."
 RL Nucleic Acids Res. 12:8407-8414(1984).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X01147; CAA25598.1; -
 DR PIR: A01966; LIHUBL.
 DR HSSP: P01703; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.
 FT DOMAIN 20 115 V SEGMENT.
 FT DOMAIN 116 130 J SEGMENT.
 FT DISULFID 41 108 BY SIMILARITY.
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 13564 MW; FA44BBL17D3A55BDF CRC64;

Query Match 81.0%; Score 470; DB 1; Length 130;
 Best Local Similarity 79.3%; Pred. No. 1,2e-36;
 Matches 88; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 QSVLTQPPSASGTPGQRTVITSCGSSSSNIGIN-ANVMYQQLPGLTAPKLLIYGNDRPSGVP 60
 DB 20 QSVLTQPPSVSAAPGQRTVITSCGSSSSNIGINDVSVYQQLPGLTAPKLLIYDNKRPSGIP 79
 QY 61 DFFSSKSGTASLAISGLQSEDEADYICAMDSLSGPVGGGKTLTVL 111
 DB 80 DFFSSKSGTASLATIGTGLTQDEADYICGTWNNSLSGWFVGGGKTLTVL 130

RESULT 5

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:21 ; Search time 194.32 Seconds

(without alignments)
98.819 Million cell updates/sec

Title: US-09-780-035-29

Perfect score: 580

Sequence: 1 QSVLTQPPSASGTPGQRTVIT.....WDDSLSGPVGGGRTLVGL 111

Scoring table: BLOSUM62

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP xvirus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	81.0	108	4 Q96SBO	Q96SBO homo sapien
2	454.5	78.4	236	4 Q96E61	Q96E61 homo sapien
3	379	65.3	112	4 Q96JD2	Q96JD2 homo sapien
4	366	63.1	116	4 Q96JD0	Q96JD0 homo sapien
5	340.5	58.7	112	4 Q96JD1	Q96JD1 homo sapien
6	319	55.0	107	4 Q9NSD6	Q9NSD6 homo sapien
7	301.5	52.0	107	4 Q9UL82	Q9UL82 homo sapien
8	293	50.5	235	11 Q99M11	Q99M11 mus musculu
9	289	49.8	233	4 Q96I69	Q96I69 homo sapien
10	278	47.9	235	11 Q91W12	Q91W12 mus musculu
11	261	45.0	106	5 Q9U410	Q9U410 schistosoma
12	260	44.8	109	4 Q9UL78	Q9UL78 homo sapien
13	256	44.1	107	4 Q9UL81	Q9UL81 homo sapien
14	255	44.0	101	11 Q9UL78	Q9UL78 mus musculu
15	255	44.0	107	4 Q96SA9	Q96SA9 homo sapien
16	253	43.6	109	4 Q9UL85	Q9UL85 homo sapien

17	248	42.8	97	11 Q9UL76	Q9UL76 mus musculu
18	247	42.6	109	4 Q9UL86	Q9UL86 homo sapien
19	244	42.1	233	11 Q91V32	Q91V32 m adult mal
20	239.5	41.3	108	4 Q9UL79	Q9UL79 homo sapien
21	237.5	40.9	108	4 Q9UL77	Q9UL77 homo sapien
22	236.5	40.8	233	11 Q91WS9	Q91WS9 mus musculu
23	235.5	40.6	108	4 Q9UL70	Q9UL70 homo sapien
24	235	40.5	109	11 Q9ET13	Q9ET13 mus musculu
25	233.5	40.3	108	4 Q9UL83	Q9UL83 homo sapien
26	231.5	39.9	107	11 Q9ER29	Q9ER29 mus musculu
27	230.5	39.7	111	11 Q920E9	Q920E9 mus musculu
28	226.5	39.1	109	6 Q9NDW5	Q9NDW5 oryctolagus
29	225.5	38.9	93	4 Q9UL76	Q9UL76 homo sapien
30	224.5	38.7	127	11 Q925S9	Q925S9 mus musculu
31	222	38.3	99	11 Q9UL74	Q9UL74 mus musculu
32	218.5	37.7	214	11 Q9RIA5	Q9RIA5 mus musculu
33	216.5	37.3	298	11 Q9QYF0	Q9QYF0 mus musculu
34	215.5	37.2	109	11 Q920E6	Q920E6 mus musculu
35	213	36.7	103	11 Q9UL80	Q9UL80 mus musculu
36	213	36.7	238	11 Q99M37	Q99M37 mus musculu
37	211.5	36.5	114	4 Q9UL80	Q9UL80 homo sapien
38	209.5	36.1	114	4 Q9UL80	Q9UL80 mus musculu
39	207.5	35.8	104	11 Q9UL82	Q9UL82 mus musculu
40	206.5	35.6	234	11 Q91WF8	Q91WF8 mus musculu
41	205.5	35.4	116	4 Q96PF6	Q96PF6 homo sapien
42	200.5	34.6	107	11 Q9JL84	Q9JL84 mus musculu
43	195.5	33.7	154	11 Q91XK2	Q91XK2 mus musculu
44	189	32.6	241	11 Q921A6	Q921A6 mus musculu
45	179.5	30.9	123	11 Q612A3	Q612A3 mus musculu

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	108 AA.
Q96SBO	Q96SBO	Q96SBO		
AC	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)			
DE	ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN			
DE	VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98375893; PubMed=9712075;			
RA	Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;			
RT	"Molecular analysis of polyclonal antibodies from			
RT	rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin			
RT	antibody V region genes."			
RL	J. Immunol. 161:2020-2031(1998).			
DR	EMBL: U96394; AAB68783.1; -			
FT	NON-TER			
SO	SEQUENCE			

Query Match 81.0% Score 470; DB 4; Length 108;
Best Local Similarity 92.9% Pred. No. 7.2e-41;
Matches 91; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY	1 QSVLTQPPSASGTPGQRTVITSCGSSSSNGINAVNMYQQLPCTAKLITYGNDQRPSPGP 60
DB	1 QSVLTQPPSASGTPGQRTVITSCGSSSSNGINAVNMYQQLPCTAKLITYRNQSPSPGP 60
QY	61 DRPSGSGTSSASLISGQSEDEADYCAAMDLSIG 98
DB	61 DRPSGSGTSSASLISGIRSEADYCAAMDRLSG 98

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:40 ; Search time 109.39 Seconds

(without alignments)
4.392 Million cell updates/sec

Title: US-09-780-035-28_COPY_21_25

Perfect score: 24

Sequence: 1 SYAMS 5

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR-71:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	76	2 H30517	Ig heavy chain V-A
2	24	100.0	90	2 S24248	Ig heavy chain V r
3	24	100.0	92	2 S56009	Ig heavy chain var
4	24	100.0	92	2 S56008	Ig heavy chain var
5	24	100.0	96	2 S20781	Ig heavy chain V r
6	24	100.0	97	1 HVM591	Ig heavy chain V r
7	24	100.0	98	2 S26889	Ig heavy chain V r
8	24	100.0	100	2 S24258	Ig heavy chain V r
9	24	100.0	101	2 S24257	Ig heavy chain V r
10	24	100.0	102	2 S14581	Ig heavy chain V r
11	24	100.0	102	2 S24260	Ig heavy chain V r
12	24	100.0	104	2 S24255	Ig heavy chain V r
13	24	100.0	105	2 S24249	Ig heavy chain V r
14	24	100.0	106	2 S24256	Ig heavy chain V r
15	24	100.0	108	2 PH1648	Ig heavy chain V r
16	24	100.0	108	2 PH1011	Ig heavy chain V r
17	24	100.0	109	2 PH1649	Ig heavy chain V r
18	24	100.0	109	2 S24254	Ig heavy chain V r
19	24	100.0	109	2 S24253	Ig heavy chain V r
20	24	100.0	110	2 S24250	Ig heavy chain V r
21	24	100.0	111	2 PH1659	Ig heavy chain V r
22	24	100.0	111	2 S40090	Ig heavy chain - m
23	24	100.0	111	2 PH1007	Ig heavy chain V r
24	24	100.0	112	2 S26327	Ig heavy chain V r
25	24	100.0	112	2 PH1647	Ig heavy chain V r
26	24	100.0	113	2 S34792	Ig heavy chain pre
27	24	100.0	113	2 S24247	Ig heavy chain V r
28	24	100.0	113	2 S25571	Ig heavy chain V r
29	24	100.0	117	1 H3H026	Ig heavy chain pre

30	24	100.0	117	2 A45953	Ig heavy chain pre
31	24	100.0	117	2 B34964	Ig heavy chain pre
32	24	100.0	118	2 S31121	Ig heavy chain - h
33	24	100.0	119	2 C36005	Ig heavy chain V r
34	24	100.0	119	2 D36005	Ig heavy chain V r
35	24	100.0	119	2 S31107	Ig heavy chain - h
36	24	100.0	119	2 S31108	Ig heavy chain - h
37	24	100.0	120	2 S48798	Ig heavy chain V r
38	24	100.0	120	2 S55538	Ig heavy chain V r
39	24	100.0	120	2 S55539	Ig heavy chain V r
40	24	100.0	120	2 S55537	Ig heavy chain V r
41	24	100.0	121	2 H27888	Ig heavy chain V r
42	24	100.0	121	2 S31113	Ig heavy chain - h
43	24	100.0	122	2 PC2398	Ig heavy chain - h
44	24	100.0	123	2 G27888	Ig heavy chain V r
45	24	100.0	123	2 S31114	Ig heavy chain - h

ALIGNMENTS

RESULT 1
H30517
Ig heavy chain V-A1 region (RVH139) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 17-Nov-1988 #sequence_revision 17-Nov-1988 #text_change 16-Aug-1996
C:Accession: H30517
R:McCormack, W.T.; Dhanarajan, P.; Roux, K.H.
J. Immunol. 141, 2063-2071, 1988
A:Title: Comparison of latent and nominal rabbit Ig VH allotype cDNA sequences.
A:Reference number: A30517; MUID:89009696
A:Accession: H30517
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-76 <MCC>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 24; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
Db 11 SYAMS 15

RESULT 2
S24248
Ig heavy chain V region (VH26) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24248
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B
A:Reference number: S24247
A:Accession: S24248
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STE>
A:Cross-references: EMBL:X67069; NTD:Q38395; PIRN:CAA47454.1; PID:Q38396
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 24; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. NO. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYAMS 5
|||||

Db 30 SYAMS 34

RESULT 3

S56009

Ig heavy chain variable region against dystrophin - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

C:Accession: S56009

R:Morris, G.E.; Nguyen, C.; Man, N.T.

Biochem. J. 309, 355-359, 1995

A:Title: Specificity and V(H) sequence of two monoclonal antibodies against the N-termin

A:Reference number: S56008; MUID:95344393

A:Accession: S56009

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <MOR>

A:Cross-references: EMBL:Z46661

C:Superfamily: immunoglobulin V region; immunoglobulin homology,

C:Keywords: heterotetramer; immunoglobulin

F:6-86/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 92;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5

|||||

Db 22 SYAMS 26

RESULT 4

S56008

Ig heavy chain variable region MANEX1B against dystrophin - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

C:Accession: S56008

R:Morris, G.E.; Nguyen, C.; Man, N.T.

Biochem. J. 309, 355-359, 1995

A:Title: Specificity and V(H) sequence of two monoclonal antibodies against the N-termin

A:Reference number: S56008; MUID:95344393

A:Accession: S56008

A:Status: preliminary

A:Molecule type: mRNA

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:6-86/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 92;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5

|||||

Db 22 SYAMS 26

RESULT 5

S20781

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20781

R:Mortari, F.; Wang, J.; Schroeder, H.W.

submitted to the EMBL Data Library, April 1992

A:Description: Analysis of human cord blood Ig heavy chain Iga and Igg repertoire.

A:Reference number: S20764

A:Accession: S20781

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-96 <MOR>

A:Cross-references: EMBL:Z11945; NID:933895; PIDN:CAA78002.1; PID:933896

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 96;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5

|||||

Db 6 SYAMS 10

RESULT 6

HVMS91

Ig heavy chain V region (914) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: J70504

R:Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: J70501; MUID:89279149

A:Accession: J70504

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-97 <LEV>

A:Experimental source: strain BALB/cJ

A>Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

F:22-95/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 100.0%; Score 24; DB 1; Length 97;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5

|||||

Db 31 SYAMS 35

RESULT 7

S26889

Ig heavy chain V region (DP-47) - human

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S26889

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o

A:Reference number: S26885; MUID:93021117

A:Accession: S26889

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TON>

A:Cross-references: EMBL:Z12347; NID:932914; PIDN:CAA78217.1; PID:932915

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

OY 1 SYAMS 5

|||||

Db 31 SYAMS 35

RESULT 8
S24258
Ig heavy chain V region (VH26-DXP1-JH4) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24258
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24258
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-100 <STE>
A:Cross-references: EMBL:X67066; NID:g38389; PIDN:CAA47451.1; PID:g38390
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-86/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 24; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
|||||
Db 19 SYAMS 23

RESULT 9
S24257
Ig heavy chain V region (VH26-DXP1-JH4) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24257
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24257
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <STE>
A:Cross-references: EMBL:X67065; NID:g38387; PIDN:CAA47450.1; PID:g38388
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-93/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 24; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
|||||
Db 26 SYAMS 30

RESULT 10
S14581
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S14581
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
Submitted to the EMBL Data Library, March 1991
A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH
A:Reference number: S14484
A:Accession: S14581
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-102 <CHE>
A:Cross-references: EMBL:X58653; NID:g51295; PIDN:CAA41510.1; PID:g51296
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 24; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
|||||
Db 23 SYAMS 27

RESULT 11
S24260
Ig heavy chain V region (VH26-DAL-JH4) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S24260
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B
A:Reference number: S24247
A:Accession: S24260
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <STE>
A:Cross-references: EMBL:X67068
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:5-87/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 24; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
|||||
Db 20 SYAMS 24

RESULT 12
S24255
Ig heavy chain V region (VH26-DLR5-JH4) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S24255
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B
A:Reference number: S24247
A:Accession: S24255
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <STE>
A:Cross-references: EMBL:X67063
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:2-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 24; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
|||||
Db 17 SYAMS 21

RESULT 13

S24249

Ig heavy chain V region (VH26-DN1-DXP1-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997

C:Accession: S24249

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

Submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24249

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <STE>

A:Cross-references: EMBL:X67070

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:10-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 105;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5

Db 25 SYAMS 29

RESULT 14

S24256

Ig heavy chain V region (VH26-DXP4-JH6) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S24256

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

Submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24256

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-106 <STE>

A:Cross-references: EMBL:X67064; NID:938385; PIDN:CA447449.1; PTD:938386

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:4-86/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 106;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5

Db 19 SYAMS 23

RESULT 15

PH1648

Ig heavy chain V region (clone 2B8) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1648

R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc

A:Reference number: PH1642; MUID:93301610

A:Accession: PH1648

A:Molecule type: mRNA

A:Residues: 1-108 <HIL>

A:Experimentally source: B cell

C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 24; DB 2; Length 108;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5

Db 23 SYAMS 27

Search completed: June 21, 2002, 09:23:41
 Job time: 494 sec

RA Matthysens G., Rabbitts T.H.;

RT "Structure and multiplicity of genes for the human immunoglobulin heavy chain variable region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
 CC -----
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 CC -----
 DR EMBL: J00236; AAA53516.1; -
 DR EMBL: M35415; AAA58735.1; -
 DR PIR: A02047; H3HU26
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 1.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;
 Query Match 100.0%; Score 24; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYAMS 5
 ID 11111
 Db 50 SYAMS 54
 RESULT 3
 RBS_ECTSI STANDARD; PRT; 139 AA.
 ID RBS_ECTSI
 AC P24395;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (Rubisco
 DE small subunit).
 GN RBS.
 OS Ectocarpus siliculosus.
 OG Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales; Ectocarpaceae;
 CC Ectocarpus.
 CC NCBI_TaxID=2880;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DILIWYN (LYNGBYE);
 RX MEDLINE=91338696; PubMed=2102375;
 RA Valentin K., Zeische K.;
 RT "Rubisco genes indicate a close phylogenetic relation between the
 RT plastids of Chromophyta and Rhodophyta.";
 RL Plant Mol. Biol. 15:575-584(1990).
 CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
 CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
 CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
 CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 CC CATALYTIC SITE.
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2 3-
 CC phospho-D-glycerate.
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
 CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
 CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X52503; CAA36744.1; -
 DR PIR: S13124; RKAS.
 DR HSP: P00866; ARUB.
 DR Wendel; 4963; ECTSL; rbcS.1.
 DR InterPro: IPR000894; Rubisco_small.
 DR Pfam: PF00101; Rubisco_small; 1.
 DR Prodom: PD000290; Rubisco_small; 1.
 KW Photosynthesis; Carbon dioxide fixation; Photorepiration; Lyase;
 KW Oxidoreductase; Monooxygenase; Chloroplast.
 SQ SEQUENCE 139 AA; 15938 MW; E316D78035F02D CRC64;
 Query Match 100.0%; Score 24; DB 1; Length 139;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYAMS 5
 ID 11111
 Db 24 SYAMS 28
 RESULT 4
 YBFL_ECOLI STANDARD; PRT; 378 AA.
 ID YBFL_ECOLI
 AC P75741; Q9R7S9; Q9R7F0;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE H repeat-associated protein in rnsC-phrB intergenic region (ORF-H2).
 GN YBFL OR B0705.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 CC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=93259920; PubMed=8387990;
 RA Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Gray J.A., Hill C.W.;
 RT "rbs elements of Escherichia coli K-12: complex composites of shared
 RT and unique components that have different evolutionary histories.";
 RL J. Bacteriol. 175:2799-2808(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick N.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alida H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 CC -1- SIMILARITY: TO OTHER H REPEAT-ASSOCIATED PROTEINS.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:17 ; Search time 194.32 Seconds

(without alignments)
4.451 Million cell updates/sec

Title: US-09-780-035-28_COPY_21_25
Sequence: 24
1 SYAMS 5

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	37	8 Q95C82	Q95C82 pterygophor
2	24	100.0	37	8 Q95C24	Q95C24 neocystitis
3	24	100.0	37	8 Q95C22	Q95C22 postelsia p
4	24	100.0	37	8 Q95C18	Q95C18 macrocystis
5	24	100.0	37	8 Q95C16	Q95C16 macrocystis
6	24	100.0	37	8 Q95C14	Q95C14 macrocystis
7	24	100.0	37	8 Q95C12	Q95C12 pelagophycu
8	24	100.0	39	8 Q97MD3	Q97MD3 petalonia b
9	24	100.0	176	8 Q9B833	Q9B833 gobiodon hi
10	24	100.0	181	2 Q9AG87	Q9AG87 vibrio para
11	24	100.0	224	11 Q88642	Q88642 rattus norv
12	24	100.0	229	11 Q9CUA3	Q9CUA3 mus musculu
13	24	100.0	271	11 Q91WL6	Q91WL6 mus musculu
14	24	100.0	316	8 Q94W65	Q94W65 eleotris sm
15	24	100.0	347	8 Q94W85	Q94W85 schindleria
16	24	100.0	347	8 Q94W84	Q94W84 schindleria

17	24	100.0	348	8 Q9TD54	Q9TD54 cynolebias
18	24	100.0	348	8 Q34217	Q34217 chalinochro
19	24	100.0	348	8 Q34825	Q34825 julidochrom
20	24	100.0	348	8 Q34873	Q34873 lampriologus
21	24	100.0	348	8 Q34883	Q34883 lepidiolum
22	24	100.0	348	8 Q35119	Q35119 neolampiro
23	24	100.0	348	8 Q35189	Q35189 neolampiro
24	24	100.0	348	8 Q36174	Q36174 telmatocoro
25	24	100.0	348	8 Q94W75	Q94W75 typhlogobin
26	24	100.0	348	8 Q94W60	Q94W60 gobiodon hi
27	24	100.0	374	2 Q87702	Q87702 bacillus me
28	24	100.0	385	17 Q9HK41	Q9HK41 thermoplasma
29	24	100.0	385	17 Q9HJ52	Q9HJ52 thermoplasma
30	24	100.0	437	11 Q9R1A4	Q9R1A4 mus musculu
31	24	100.0	485	10 Q9S0H2	Q9S0H2 arabidopsis
32	24	100.0	487	11 Q99KA4	Q99KA4 mus musculu
33	24	100.0	518	2 Q66746	Q66746 mus musculu
34	24	100.0	572	2 Q9R954	Q9R954 campylobact
35	24	100.0	572	2 Q9R951	Q9R951 campylobact
36	24	100.0	575	2 Q85181	Q85181 campylobact
37	24	100.0	576	2 Q9RF25	Q9RF25 campylobact
38	24	100.0	589	11 Q9SEB8	Q9SEB8 rattus norv
39	24	100.0	589	11 Q9QZC6	Q9QZC6 rattus norv
40	24	100.0	630	2 P66752	P66752 campylobact
41	24	100.0	665	16 Q9PIN3	Q9PIN3 campylobact
42	24	100.0	906	16 Q98W49	Q98W49 thizobium l
43	24	100.0	1432	10 Q23230	Q23230 arabidopsis
44	24	100.0	28	8 Q95DU2	Q95DU2 splachnidin
45	21	87.5	30	8 Q95EF1	Q95EF1 asteronema

ALIGNMENTS

RESULT	ID	Q95C82	PRELIMINARY:	PRT:	37 AA.
AC	Q95C82	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE SMALL SUBUNIT (FRAGMENT).				
GN	RBOS.				
OS	Pterygophora californica.				
OG	Chloroplast.				
OC	Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Alariaceae;				
OX	Pterygophora.				
OX	NCBI_TaxID=169782;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Yoon H.S., Lee J.Y., Boo S.M., Bhattacharya D.;				
RT	"Phylogeny of Alariaceae, Laminariaceae, and Lessoniaceae				
RT	(Phaeophyceae) Based on Plastid-Encoded Rubisco Spacer and Nuclear-				
RT	Encoded rns Sequence Comparisons."				
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF318965; AAL08869.1; -.				
KW	Chloroplast.				
FT	NON_TER				
FT	SEQUENCE 37 AA: 4267 MW: EFP46BFBEC71AAA CRC64;				

Query Match 100.0%; Score 24; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 SYAMS 5
DB	24 SYAMS 28
RESULT	2
Q95C24	PRELIMINARY;
ID	Q95C24
	PRT; 37 AA.

AC 095C24: 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE SMALL SUBUNIT (FRAGMENT).
 GN RBCS.
 OS Nereocystis luetkeana.
 OC Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Lessoniaceae;
 OC Nereocystis.
 OX NCBI_TaxID=117523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoon H.S., Lee J.Y., Boo S.M., Bhattacharya D.;
 RT "Phylogeny of Alariaceae, Laminariaceae, and Lessoniaceae
 (Phaeophyceae) Based on Plastid-Encoded Rubisco Spacer and Nuclear-
 RT Encoded ITS Sequence Comparisons."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF318994; AAL08927.1; -
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 37 AA; 4280 MW; A52E0BEFBE70A70 CRC64;

Query Match: 100.0%; Score 24; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SYAMS 5
 DB 24 SYAMS 28

RESULT 3
 ID 095C22 PRELIMINARY: PRT: 37 AA.
 AC 095C22: 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE SMALL SUBUNIT (FRAGMENT).
 GN RBCS.
 OS Postelsia palmaeformis.
 OC Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Lessoniaceae;
 OC Postelsia.
 OX NCBI_TaxID=105414;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoon H.S., Lee J.Y., Boo S.M., Bhattacharya D.;
 RT "Phylogeny of Alariaceae, Laminariaceae, and Lessoniaceae
 (Phaeophyceae) Based on Plastid-Encoded Rubisco Spacer and Nuclear-
 RT Encoded ITS Sequence Comparisons."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF318995; AAL08929.1; -
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 37 AA; 4280 MW; A52E0BEFBE70A70 CRC64;

Query Match: 100.0%; Score 24; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
 DB 24 SYAMS 28

RESULT 4
 ID 095C18 PRELIMINARY: PRT: 37 AA.
 AC 095C18: 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE SMALL SUBUNIT (FRAGMENT).
 GN RBCS.
 OS Nereocystis integrifolia.
 OC Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Lessoniaceae;
 OC Nereocystis.
 OX NCBI_TaxID=169774;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoon H.S., Lee J.Y., Boo S.M., Bhattacharya D.;
 RT "Phylogeny of Alariaceae, Laminariaceae, and Lessoniaceae
 (Phaeophyceae) Based on Plastid-Encoded Rubisco Spacer and Nuclear-
 RT Encoded ITS Sequence Comparisons."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF318997; AAL08933.1; -
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 37 AA; 4280 MW; A52E0BEFBE70A70 CRC64;

Query Match: 100.0%; Score 24; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 SYAMS 5
 DB 24 SYAMS 28

RESULT 5
 ID 095C16 PRELIMINARY: PRT: 37 AA.
 AC 095C16: 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE SMALL SUBUNIT (FRAGMENT).
 GN RBCS.
 OS Nereocystis pyrifera (Giant kelp).
 OC Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Lessoniaceae;
 OC Nereocystis.
 OX NCBI_TaxID=35122;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoon H.S., Lee J.Y., Boo S.M., Bhattacharya D.;
 RT "Phylogeny of Alariaceae, Laminariaceae, and Lessoniaceae
 (Phaeophyceae) Based on Plastid-Encoded Rubisco Spacer and Nuclear-
 RT Encoded ITS Sequence Comparisons."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF318998; AAL08935.1; -
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 37 AA; 4280 MW; A52E0BEFBE70A70 CRC64;

Query Match: 100.0%; Score 24; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
 DB 24 SYAMS 28

RESULT 6
 ID 095C14 PRELIMINARY: PRT: 37 AA.
 AC 095C14: 01-DEC-2001 (Tremblrel. 19, Created)

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:15 ; Search time 245.49 seconds
(without alignments)

2.262 Million cell updates/sec

Title: US-09-780-035-28_COPY_21_25

Perfect score: 24

Sequence: 1 SYAMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database :
1: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	5	AA50319	MAB NFS2 heavy cha
2	24	100.0	5	AA57962	MAB NFS2 heavy cha
3	24	100.0	5	AA70460	VH sequence of ant
4	24	100.0	5	AA16650	Anti-cancer specif
5	24	100.0	5	AA95212	Anti-platelet glyco
6	24	100.0	5	AA32229	G-CSF agonist mab1
7	24	100.0	5	AA99146	Human scfv clone 2
8	24	100.0	11	AA93625	CTLA-4 VLD CDR 100
9	24	100.0	18	AA93552	CTLA-4 VLD CDR1 re
10	24	100.0	29	AA92481	Clone selected aft
11	24	100.0	29	AA92482	Clone selected aft

12	24	100.0	55	20	AA92515	Clone selected aft
13	24	100.0	56	20	AA92513	Clone selected aft
14	24	100.0	56	20	AA92514	Clone selected aft
15	24	100.0	56	20	AA92519	Clone selected aft
16	24	100.0	56	20	AA92521	Clone selected aft
17	24	100.0	56	20	AA92523	Clone selected aft
18	24	100.0	56	20	AA92498	Clone selected aft
19	24	100.0	56	20	AA92499	Clone selected aft
20	24	100.0	56	20	AA92500	Clone selected aft
21	24	100.0	56	20	AA92501	Clone selected aft
22	24	100.0	56	20	AA92502	Clone selected aft
23	24	100.0	56	20	AA92503	Clone selected aft
24	24	100.0	56	20	AA92505	Clone selected aft
25	24	100.0	56	20	AA92507	Clone selected aft
26	24	100.0	56	20	AA92510	Clone selected aft
27	24	100.0	56	20	AA92511	Clone selected aft
28	24	100.0	56	20	AA92480	Clone selected aft
29	24	100.0	56	20	AA92483	Clone selected aft
30	24	100.0	56	20	AA92489	Clone selected aft
31	24	100.0	56	20	AA92490	Clone selected aft
32	24	100.0	56	20	AA92491	Clone selected aft
33	24	100.0	56	20	AA92492	Clone selected aft
34	24	100.0	56	20	AA92473	Clone selected aft
35	24	100.0	56	20	AA92475	Clone selected aft
36	24	100.0	56	20	AA92476	Clone selected aft
37	24	100.0	56	20	AA92477	Clone selected aft
38	24	100.0	56	20	AA92479	Clone selected aft
39	24	100.0	72	22	AA923728	Human EST encoded
40	24	100.0	88	22	AA923728	Mouse germline hea
41	24	100.0	89	22	AA923728	Mouse germline hea
42	24	100.0	89	22	AA923728	SPA-reactive VH re
43	24	100.0	98	21	AA940093	Anti-hlil2 antibod
44	24	100.0	98	21	AA940097	Anti-hlil2 antibod
45	24	100.0	98	21	AA950972	Human FVIII antibo

ALIGNMENTS

RESULT 1
AA50319 AAR50319 standard; Protein; 5 AA.
XX
AC AAR50319;
XX
DT 05-OCT-1994 (first entry)
XX
DE MAB NFS2 heavy chain variable region CDR1 (modified).
XX
KW Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein;
KW murine; variable; light; heavy; chain; malaria.
XX
XX Synthetic.
XX OS
XX PN WO9405690-A.
XX PD 17-MAR-1994.
XX PF 08-SEP-1993; 93WO-US08435.
XX PR 09-SEP-1992; 92US-0941654.
XX
XX (SMIR) SMITHKLINE BEECHAM CORP.
XX (USNA) US SEC OF ARMY.
XX (USNA) US SEC OF NAVY.
XX
XX Charenyit Y, Hoffman S, Hurlie M, Rosenberg M;
XX Sedoff JC, Sylvester DR, Gross MS;
XX WPI; 1994-101115/12.
XX N-PDB; AAQ44829.
XX

PT New engineered antibodies and fusion proteins for preventing
 PT Plasmodium infection - contg. murine antibody CDR sequences, and
 PT corresp. nucleic acid, vectors and transformed cells
 XX
 PS Claim 16; Page 83; 98pp; English.
 XX
 CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)
 CC variable light chain and variable heavy chain sequences
 CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
 CC its variable chain peptides, CDRs, functional fragments,
 CC Fab fragments, and analogs are useful in prodn. of fusion
 CC proteins, esp. engineered antibodies. These prods. are
 CC used to protect humans against Plasmodium infections.
 XX
 SQ Sequence 5 AA;
 XX
 Query Match 100.0%; Score 24; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYAMS 5
 Db 1 syams 5
 XX
 RESULT 2
 AAR57962
 ID AAR57962 standard; Protein; 5 AA.
 XX
 AC AAR57962;
 XX
 DT 05-OCT-1994 (first entry)
 XX
 DE MAb NFS2 heavy chain variable region CDRL.
 XX
 KM Monoclonal antibody; Plasmodium falciparum; CDR;
 KM complementarity determining region; fusion protein;
 KM murine; variable; light; heavy; chain; malaria.
 XX
 OS Plasmodium falciparum.
 XX
 PN W09405690-A.
 XX
 PD 17-MAR-1994.
 XX
 PF 08-SEP-1993; 93WO-US08435.
 XX
 PR 09-SEP-1992; 92US-0941654.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (USNA) US SEC OF ARMY.
 PA (USNA) US SEC OF NAVY.
 XX
 PI Chaoenvit Y, Hoffman S, Hurle M, Rosenberg M;
 PI Saoff JC, Sylvestre DR, Gross MS;
 DR WPI; 1994-101115/12.
 DR N-PSDB; AAQ44835.
 XX
 PT New engineered antibodies and fusion proteins for preventing
 PT Plasmodium infection - contg. murine antibody CDR sequences, and
 PT corresp. nucleic acid, vectors and transformed cells
 XX
 PS Disclosure; Page 67; 98pp; English.
 XX
 CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)
 CC variable light chain and variable heavy chain sequences
 CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
 CC its variable chain peptides, CDRs, functional fragments,
 CC Fab fragments, and analogs are useful in prodn. of fusion
 CC proteins, esp. engineered antibodies. These prods. are
 CC used to protect humans against Plasmodium infections.

XX
 SQ Sequence 5 AA;
 XX
 Query Match 100.0%; Score 24; DB 15; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYAMS 5
 Db 1 syams 5
 XX
 RESULT 3
 AAR70460
 ID AAR70460 standard; peptide; 5 AA.
 XX
 AC AAR70460;
 XX
 DT 27-OCT-1995 (first entry)
 XX
 DE VH sequence of anti-KC-4 monoclonal antibody (IID-D9-JH3) corresp. to
 DE complementarity determining region 1 (CDRL).
 XX
 KM Anti-KC-4 antibody; monoclonal antibody; cancer.
 XX
 OS Synthetic.
 XX
 PN W09510776-A.
 XX
 PD 20-APR-1995.
 XX
 PF 16-NOV-1993; 93WO-US11444.
 XX
 PR 08-OCT-1993; 93US-0134346.
 XX
 PA (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
 PA Ceriani RL, Docouto JFR, Peterson JA;
 PI WPI; 1995-161912/21.
 DR N-PSDB; AAQ87532.
 XX
 PT New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells, in vivo imaging, ex-vivo purging and treatment of
 PT cancers
 XX
 PS Example; Table 15, page 32; 61pp; English.
 XX
 CC The cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL
 CC were prepared by PCR from polyadenylated RNA isolated from 100
 CC million KC-4 hybridoma cells. All clones were obtd. from independent
 CC PCRs. The sequences of the primers are given in AAQ87519-Q87526.
 CC Primers are specific for either the leader peptide region or for the
 CC constant regions. The PCR products were cloned, without prior
 CC purification, into pCR1000 (Invitrogen) and sequenced in both directions.
 CC The VH DNA sequence and its derived protein sequences are shown
 CC in AAQ87532, and AAR70458-R70466. VH belongs to group IIId. CDR3 and
 CC FR4 resulted from a genomic recombination involving minigenes D9
 CC and JH3.
 XX
 SQ Sequence 5 AA;
 XX
 Query Match 100.0%; Score 24; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SYAMS 5
 Db 1 syams 5

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RESULT 4
AAWI6650
ID AAWI6650 standard; Peptide; 5 AA.
XX
AC AAWI6650;
XX
DT 29-JAN-1998 (first entry)
XX
DE Anti-cancer specific antigen MAb heavy chain CDR1.
XX
KM Heavy chain; variable region; cancer specific antigen; human;
KM monoclonal antibody; hMab; diagnosis; cancer; immunotherapy;
KM purification; complementarity determining region 1; CDR1.
XX
OS Homo sapiens.
XX
PN JP09098786-A.
XX
PD 15-APR-1997.
XX
PF 06-OCT-1995; 95JP-0284400.
XX
PR 06-OCT-1995; 95JP-0284400.
XX
PA (MOMI ) MORINAGA & CO LTD.
PA (SHKU ) SHINGIUTSU JIGYODAN.
XX
DR WPI; 1997-275445/25.
XX
DR N-PSDB; AAT66782.
XX
PT cDNA encoding human monoclonal antibody - useful in medicine, or to
PT purify cancer specific antigen
XX
PS Claim 9; Fig 11; 7pp; Japanese.
XX
CC The present sequence is the heavy chain complementarity
CC determining region 1 of an anti-cancer specific antigen human
CC monoclonal antibody (hMab). The hMab can be used in medicine, e.g.
CC clinical diagnosis of cancer or immunotherapy, or to purify cancer
CC specific antigen. The industrial scale production of large amounts
CC of the hMab is made feasible by genetic engineering using the hMab
CC cDNA.
XX
SQ Sequence 5 AA:
XX
Query Match 100.0%; Score 24; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYAMS 5
Db 1 syams 5

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```

RESULT 5
AAW95212
ID AAW95212 standard; Peptide; 5 AA.
XX
AC AAW95212;
XX
DT 29-AUG-2000 (first entry)
XX
DE Anti-platelet glycoprotein Ib human H1b-3 VH CDR1.
XX
KM Variable heavy chain; single chain antibody; scFv; human; H1b-3;
KM glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
KM antithrombotic; thrombus; therapy; diagnostic; CDR1;
KM complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO200026667-A1.
XX

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XX
PD 11-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US25495.
XX
PR 30-OCT-1998; 98US-0106275.
XX
PA (MILL/) MILLER J L.
XX
PI Miller JL;
XX
DR WPI; 2000-365744/31.
XX
PT Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX
PS Claim 14; Fig 7; 89pp; English.
XX
CC The present sequence is that of complementarity determining region
CC 1 (CDR1) of the heavy chain variable region (VH) of human
CC single chain antibody (scFv) H1b-3 (see AAW95212), which is directed
CC against platelet glycoprotein Ib (GPIb). The H1b series of scFv
CC is isolated from a human synthetic VH and VL scFv library on the
CC basis of their binding to platelet GPIb. Whether displayed as
CC surface proteins on a phagemid or secreted as free scFv by
CC Escherichia coli, the H1b scFv clones are capable of inhibiting
CC von Willebrand factor-dependent aggregation of platelets. The scFv
CC are composed of native human protein sequences and are therefore
CC attractive potential reagents for therapeutic purposes. They
CC provide a new class of antithrombotic agents, useful for the
CC prevention of platelet-dependent thrombi in diseased arteries,
CC bypass grafts, dialysis etc., and can also be used as diagnostic
CC reagents. Methods of inhibiting aggregation of platelets, of
CC binding human platelet GPIb alpha and of selecting a VH or VL
CC region of an antibody that inhibits platelet aggregation are
CC claimed. Fragments of the scFv VH or VL chain, including CDR
CC fragments, are also claimed.
XX
SQ Sequence 5 AA:
XX
Query Match 100.0%; Score 24; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYAMS 5
Db 1 syams 5

```

```

RESULT 6
AAW32229
ID AAW32229 standard; Peptide; 5 AA.
XX
AC AAW32229;
XX
DT 15-FEB-2000 (first entry)
XX
DE G-CSF agonist mAb174-74-11 heavy chain variable region CDR1.
XX
KM Granulocyte colony stimulating factor receptor; G-CSF; mouse;
KM monoclonal antibody; agonist; screening; neutropenia; therapy;
KM complementarity determining region; CDR; mAb174-74-11.
XX
OS Mus musculus.
XX
PN WO955735-A1.
XX
PD 04-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09466.
XX

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PR 30-APR-1998; 98US-0083575.
 XX
 PA (TANO-) TANOX INC.
 XX
 PI Ni B, Sun BNC, Sun CRY;
 XX
 DR WPI; 2000-052805/04.
 XX
 PT Treatment of neutropenia by stimulating proliferation of neutrophilic
 PT cell lineage progenitors -
 XX
 PS Claim 14; Page 30; 64pp; English.
 XX
 CC The present sequence represents complementarily determining region
 CC 1 (CDR1) of the heavy chain variable region of murine monoclonal
 CC antibody mAb174-74-11. This antibody is an example of an agonist
 CC molecule that specifically binds to or interacts with human
 CC granulocyte colony stimulating factor (G-CSF) receptor to stimulate
 CC cell proliferation and differentiation, especially by dimerizing
 CC the receptor or activating phosphorylation of kinases associated
 CC with the receptor. Agonist antibodies can be used to stimulate
 CC proliferation of G-CSF-dependent cells, e.g. to differentiate
 CC leading to a repopulation of neutrophilic granulocyte lineage
 CC cells, especially to treat neutropenia (claimed). They can also
 CC be used to detect human G-CSF receptor immunologically.
 CC
 XX
 SO Sequence 5 AA;

Query Match 100.0%; Score 24; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
 |||||
 Db 1 syams 5

RESULT 7
 AAB99146
 ID AAB99146 standard; Peptide; 5 AA.
 XX
 AC AAB99146;
 XX
 DT 31-AUG-2001 (first entry)
 XX
 DE Human scFv clone 291J1 CDRH1 peptide fragment.
 XX
 KM Human; immunoglobulin screening; enzyme screening; inflammation;
 KM allergy; cancer; infection; autoimmune disorder; scFv.
 XX
 OS Homo sapiens.
 XX
 PN WO200140803-A1.
 XX
 PD 07-JUN-2001.
 XX
 PE 04-DEC-2000; 2000WO-GB04638.
 XX
 PR 03-DEC-1999; 99GB-0028787.
 XX
 PA (DIVE-) DIVERSYS LTD.
 XX
 PI Holt LJ, De Wildt RMT, Tomlinson I;
 XX
 DR WPI; 2001-374956/39.
 XX
 PT Screening repertoire of polypeptides, e.g. immunoglobulin molecules, by
 PT translating polypeptides in close proximity to target molecules so that
 PT repertoire members that interact with the molecules are identified -
 XX
 PS Example 1; Page 35; 59pp; English.
 XX

CC The present invention relates to a method for screening a repertoire of
 CC polypeptides to identify members which interact with target molecules.
 CC The method is useful for screening, for example, immunoglobulin molecules
 CC and enzymes. The method is also applicable for screening two repertoire
 CC polypeptides against one another to isolate specific binding pairs.
 CC Molecules selected by the methods are useful in diagnostic, prophylactic
 CC and therapeutic procedures for preventing, suppressing or treating
 CC inflammatory states, allergic hypersensitivity, cancer, bacterial or
 CC viral infection and autoimmune disorders. The present sequence is a
 CC peptide fragment of a human single chain Fv (scFv) clone, which was used
 CC in an example from the present invention.
 CC
 XX
 SO Sequence 5 AA;

Query Match 100.0%; Score 24; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
 |||||
 Db 1 syams 5

RESULT 8
 AAY39625
 ID AAY39625 standard; peptide; 11 AA.
 XX
 AC AAY39625;
 XX
 DT 23-NOV-1999 (first entry)
 XX
 DE CTLA-4 VLD CDR loop replacement.
 XX
 KM CTLA-4; cytotoxic T-lymphocyte associated antigen 4; binding agent; VLD;
 KM variable-like domain; human; diagnosis; cancer; blood clot.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945110-A1.
 XX
 PD 10-SEP-1999.
 XX
 PE 05-MAR-1999; 99WO-AU00136.
 XX
 PR 06-MAR-1998; 98AU-0002210.
 XX
 PA (DIAT-) DIATECH PTY LTD.
 XX
 PI Coia G, Galanis M, Hudson PJ, Irving RA, Nuttall SD;
 XX
 DR WPI; 1999-551040/46.
 XX
 PT New binding agent comprising monomeric V-like domain in which at least
 PT one complementarity determining region loop is modified, useful for
 PT diagnosis of cancer -
 XX
 PS Example 6; Fig 6; 117pp; English.
 XX

CC This sequence is variable-like domain (VLD) of the human cytotoxic
 CC T-lymphocyte associated antigen 4 (CTLA-4) CDR loop replacement, used
 CC in the binding agent of the invention. The binding agent (I) comprises at
 CC least one monomeric VLD that is derived from a non-antibody ligand and
 CC has at least one CDR (complementarity determining region) loop sequence,
 CC or part of it, modified or replaced so that, compared to unmodified VLD,
 CC its solubility is increased and/or the size is altered and/or a
 CC disulphide bond is created within, or between, one or more CDR loops. (I)
 CC are used for diagnosis, e.g. in vivo detection/localisation of cancer,
 CC blood clots etc., also in vitro when immobilised on solid supports or
 CC biosensors and therapeutically. Modified VLD may have binding affinity
 CC for drugs, steroids, pesticides, antigens, growth factors, tumour
 CC markers, cell or viral proteins. Modification of VLD improves solubility

CC and alters binding specificity. Since VLD are derived from human
 CC proteins, the need for a humanizing step (to avoid adverse immune
 CC responses) is avoided, and modification also improves expression in
 CC Escherichia coli.

XX Sequence 11 AA;

Query Match 100.0%; Score 24; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
 |||||
 Db 7 syams 11

RESULT 9

AA939552 ID AAY39552 standard; peptide; 18 AA.

XX AC AAY39552;

XX DF 23-NOV-1999 (first entry)

XX DE CTLA-4 VLD CDRI region variant.

XX KM CTLA-4; cytotoxic T-lymphocyte associated antigen 4; binding agent; VLD;
 XX KW variable-like domain; human; diagnosis; cancer; blood clot.

XX OS Homo sapiens.

XX PN WO945110-A1.

XX PD 10-SEP-1999.

XX PF 05-MAR-1999; 99WO-AU00136.

XX PR 06-MAR-1998; 98AU-0002210.

XX PA (DIAT-) DIATECH PRY LTD.

XX PI Cola G, Galanis M, Hudson PJ, Irving RA, Nuttall SD;

XX DR WPI; 1999-551040/46.

XX PT New binding agent comprising monomeric V-like domain in which at least
 XX PT one complementarity determining region loop is modified, useful for
 XX PT diagnosis of cancer

XX PS Example 1; Page 18; 117pp; English.

XX CC This sequence is a variant of the CDRI of the variable-like domain (VLD)
 CC of the human cytotoxic T-lymphocyte associated antigen 4 (CTLA-4), used
 CC in the binding agent of the invention. The binding agent (I) comprises at
 CC least one monomeric VLD that is derived from a non-antibody ligand and
 CC has at least one CDR (complementarity determining region) loop sequence,
 CC or part of it, modified or replaced so that, compared to unmodified VLD,
 CC its solubility is increased and/or the size is altered and/or a
 CC disulphide bond is created within, or between, one or more CDR loops. (1)
 CC are used for diagnosis, e.g. in vivo detection/localisation of cancer,
 CC blood clots etc., also in vitro when immobilised on solid supports or
 CC biosensors and therapeutically. Modified VLD may have binding affinity
 CC for drugs, steroids, pesticides, antigens, growth factors, tumour
 CC markers, cell or viral proteins. Modification of VLD improves solubility
 CC and alters binding specificity. Since VLD are derived from human
 CC proteins, the need for a humanizing step (to avoid adverse immune
 CC responses) is avoided, and modification also improves expression in
 CC Escherichia coli.

XX XX Sequence 18 AA;

Query Match 100.0%; Score 24; DB 20; Length 18;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
 |||||
 Db 14 syams 18

RESULT 10

AA02481 ID AAY02481 standard; Protein; 29 AA.

XX AC AAY02481;

XX DT 15-JUL-1999 (first entry)

XX DE Clone selected after panning a NAK library of the invention.

XX KW Screening; functional polypeptide; ligand; non-functional;
 XX KW enrichment; single chain antibody; ScFv.

XX OS Synthetic.

XX PN WO9920749-A1.

XX PD 29-APR-1999.

XX PF 20-OCT-1998; 98WO-GB03135.

XX PR 21-NOV-1997; 97US-0066729.

XX PR 20-OCT-1997; 97GB-0022131.

XX PR 13-NOV-1997; 97US-0065428.

XX PA (MEDI-) MEDICAL RES COUNCIL.

XX PI Tomlinson I, Winter G;

XX DR WPI; 1999-288302/24.

XX PT Screening for functional polypeptides which bind a ligand

XX PS Example 3; Fig 4; 67pp; English.

XX CC The specification describes a method for screening for functional
 CC polypeptides which bind a ligand. The method comprises contacting a
 CC repertoire of polypeptides with a generic ligand, and then screening
 CC selected functional polypeptides with a target ligand. The method
 CC permits the removal from a chosen repertoire of polypeptides, those
 CC which are non-functional, e.g. as a result of the introduction of
 CC frame-shift mutations, stop codons, folding mutants or expression
 CC mutants which would be or are incapable of binding to any target
 CC ligand. The method also permits the enrichment of a chosen repertoire
 CC of polypeptides for those polypeptides which are functional, well folded
 CC and highly expressed. The polypeptides obtained can be used in
 CC diagnostic, prophylactic and therapeutic procedures. AAY02473-002525
 CC represent clones selected after panning primary and somatic NAK
 CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
 CC NIP-BSA and hen egg lysozyme).

XX XX Sequence 29 AA;

Query Match 100.0%; Score 24; DB 20; Length 29;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYAMS 5
 |||||
 Db 1 syams 5

RESULT 11

```

AY02482 ID AY02482 standard; Protein; 29 AA.
XX AC AAY02482;
XX DT 15-JUL-1999 (first entry)
XX DE Clone selected after panning a NNK library of the invention.
XX KW Screening; functional polypeptide; ligand; non-functional;
XX RV enrichment; single chain antibody; scfv.
XX OS Synthetic.
XX PN WO9920749-A1.
XX PD 29-APR-1999.
XX PF 20-OCT-1998; 98WO-GB03135.
XX PR 21-NOV-1997; 97US-0066729.
XX PR 20-OCT-1997; 97GB-0022131.
XX PR 13-NOV-1997; 97US-0065428.
XX PA (MEDICAL RES COUNCIL.
XX PL Tomlinson I, Winter G;
XX DR WPI; 1999-288302/24.
XX PT Screening for functional polypeptides which bind a ligand
XX PS Example 3; Fig 4; 67pp; English.
XX CC The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in
CC diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525
CC represent clones selected after panning procedures. AAY02473-Y02525
CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
CC NIP-BSA and hen egg lysozyme).
XX SQ Sequence 29 AA;

Query Match Best Local Similarity 100.0%; Score 24; DB 20; Length 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
Db |||||
1 sYams 5

RESULT 12
AAY02515 ID AAY02515 standard; Protein; 55 AA.
XX AC AAY02515;
XX DT 15-JUL-1999 (first entry)
XX DE Clone selected after panning a NNK library of the invention.
XX KW Screening; functional polypeptide; ligand; non-functional;

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KW      enrichment; single chain antibody; scFv.
OS      Synthetic.
PN      WO9920749-A1.
PD      29-APR-1999.
PF      20-OCT-1998; 98WO-GB03135.
PR      21-NOV-1997; 97US-0066729.
PR      20-OCT-1997; 97GB-0022131.
PR      13-NOV-1997; 97US-0065428.
PA      (MEDT-) MEDICAL RES COUNCIL.
XX      Tomlinson I, Winter G;
XX      WPI, 1999-288302/24.
XX      Screening for functional polypeptides which bind a ligand
XX      Example 3; Fig 4; 67pp; English.
XX      The specification describes a method for screening for functional
XX      polypeptides which bind a ligand. The method comprises contacting a
XX      repertoire of polypeptides with a generic ligand, and then screening
XX      selected functional polypeptides with a target ligand. The method
XX      permits the removal from a chosen repertoire of polypeptides, those
XX      which are non-functional, e.g. as a result of the introduction of
XX      frame-shift mutations, stop codons, folding mutants or expression
XX      mutants which would be or are incapable of binding to any target
XX      ligand. The method also permits the enrichment of a chosen repertoire
XX      of polypeptides for those polypeptides which are functional, well folded
XX      and highly expressed. The polypeptides obtained can be used in
XX      diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525
XX      represent clones selected after panning primary and somatic NK
XX      libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
XX      NIP-B5A and hen egg lysozyme).
XX      Sequence 55 AA:
SQ
      Query Match 100.0%; Score 24; DB 20; Length 55;
      Best Local Similarity 100.0%; Pred. No. 35;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 SYAMS 5
      1
      |||||
DB      1 syams 5
      1

RESULT 13
AAY02513
AAY02513 standard; Protein: 56 AA.
XX      AAY02513;
XX      AC
XX      15-JUL-1999 (first entry)
XX      DT
DE      Clone selected after panning a NNK library of the invention.
XX      Screening; functional polypeptide; ligand; non-functional;
XX      enrichment; single chain antibody; scFv.
XX      KW
XX      Synthetic.
XX      OS
XX      WO9920749-A1.
XX      PN
XX      29-APR-1999.
XX      PD
XX      20-OCT-1998; 98WO-GB03135.
XX

```



```

PR 21-NOV-1997; 97US-0066729.
PR 20-OCT-1997; 97GB-0022131.
PR 13-NOV-1997; 97US-0065428.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Tomlinson I, Winter G;
XX
DR WPI; 1999-288302/24.
XX
PT Screening for functional polypeptides which bind a ligand
XX
PS Example 3; Fig 4; 67pp; English.
XX
CC The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in
CC diagnostic, prophylactic and therapeutic procedures. AA02473-Y02525
CC represent clones selected after panning primary and somatic NKK
CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
CC NIP-BSA and hen egg lysozyme).
XX
SQ Sequence 56 AA;

Query Match 100.0%; Score 24; DB 20; Length 56;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
   |||||
   1 syams 5
Db

RESULT 14
AA02514
ID AA02514 standard; Protein; 56 AA.
XX
AC AA02514;
XX
DT 15-JUL-1999 (first entry)
XX
DE Clone selected after panning a NNK library of the invention.
XX
KM Screening; functional polypeptide; ligand; non-functional;
KM enrichment; single chain antibody; ScFv.
OS Synthetic.
XX
PN WO9920749-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-GB03135.
XX
PR 21-NOV-1997; 97US-0066729.
PR 20-OCT-1997; 97GB-0022131.
PR 13-NOV-1997; 97US-0065428.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Tomlinson I, Winter G;
XX
DR WPI; 1999-288302/24.
XX

```

```

PT Screening for functional polypeptides which bind a ligand
XX
PS Example 3; Fig 4; 67pp; English.
XX
CC The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in
CC diagnostic, prophylactic and therapeutic procedures. AA02473-Y02525
CC represent clones selected after panning primary and somatic NKK
CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
CC NIP-BSA and hen egg lysozyme).
XX
SQ Sequence 56 AA;

Query Match 100.0%; Score 24; DB 20; Length 56;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
   |||||
   1 syams 5
Db

RESULT 15
AA02519
ID AA02519 standard; Protein; 56 AA.
XX
AC AA02519;
XX
DT 15-JUL-1999 (first entry)
XX
DE Clone selected after panning a NNK library of the invention.
XX
KM Screening; functional polypeptide; ligand; non-functional;
KM enrichment; single chain antibody; ScFv.
OS Synthetic.
XX
PN WO9920749-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-GB03135.
XX
PR 21-NOV-1997; 97US-0066729.
PR 20-OCT-1997; 97GB-0022131.
PR 13-NOV-1997; 97US-0065428.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Tomlinson I, Winter G;
XX
DR WPI; 1999-288302/24.
XX
PT Screening for functional polypeptides which bind a ligand
XX
PS Example 3; Fig 4; 67pp; English.
XX
CC The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of

```

CC frame-shift mutations, stop codons, folding mutants or expression
 CC mutants which would be or are incapable of binding to any target
 CC ligand. The method also permits the enrichment of a chosen repertoire
 CC of polypeptides for those polypeptides which are functional, well folded
 CC and highly expressed. The polypeptides obtained can be used in
 CC diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525
 CC represent clones selected after panning primary and somatic NNK
 CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
 CC NIP-BSA and hen egg lysozyme).
 CC
 XX

SQ Sequence 56 AA;

Query Match 100.0%; Score 24; DB 20; Length 56;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
 |||||
 Db 1 syams 5

Search completed: June 21, 2002, 09:20:15
 Job time: 428 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:45 ; Search time 84.18 Seconds
(without alignments)
1.451 Million cell updates/sec

Title: US-09-780-035-28_COPY_21_25
Perfect score: 24
Sequence: 1 SYAMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/2/1aa/3A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	5	1 US-07-977-696C-38	Sequence 38, Appl
2	24	100.0	5	1 US-08-129-930B-38	Sequence 38, Appl
3	24	100.0	5	4 US-08-134-346A-25	Sequence 25, Appl
4	24	100.0	5	4 US-08-976-288A-38	Sequence 38, Appl
5	24	100.0	5	5 PCT-US93-08435-16	Sequence 16, Appl
6	24	100.0	5	5 PCT-US93-08435-33	Sequence 33, Appl
7	24	100.0	10	1 US-08-208-886C-86	Sequence 86, Appl
8	24	100.0	10	1 US-08-704-744-88	Sequence 88, Appl
9	24	100.0	10	1 US-08-469-557-67	Sequence 67, Appl
10	24	100.0	10	2 US-08-290-793B-67	Sequence 67, Appl
11	24	100.0	35	2 US-08-765-179B-1	Sequence 1, Appl
12	24	100.0	98	2 US-08-428-197-48	Sequence 48, Appl
13	24	100.0	98	5 PCT-US93-10555-48	Sequence 48, Appl
14	24	100.0	102	2 US-08-273-146-65	Sequence 65, Appl
15	24	100.0	110	1 US-08-211-202-117	Sequence 117, App
16	24	100.0	113	3 US-08-974-899-6	Sequence 6, Appl
17	24	100.0	115	3 US-08-483-749A-6	Sequence 6, Appl
18	24	100.0	116	2 US-08-428-197-2	Sequence 2, Appl
19	24	100.0	116	5 PCT-US93-10555-2	Sequence 2, Appl
20	24	100.0	117	3 US-08-545-809A-109	Sequence 109, App
21	24	100.0	117	4 US-08-983-607-46	Sequence 46, Appl
22	24	100.0	117	4 US-09-157-370-1	Sequence 1, Appl
23	24	100.0	118	2 US-08-652-816A-12	Sequence 12, Appl
24	24	100.0	118	5 PCT-US93-08435-10	Sequence 10, Appl
25	24	100.0	120	4 US-09-025-769B-38	Sequence 38, Appl
26	24	100.0	120	4 US-09-025-769B-63	Sequence 63, Appl
27	24	100.0	121	1 US-08-339-582-2	Sequence 2, Appl

28	24	100.0	122	2 US-07-934-373C-21	Sequence 21, Appl
29	24	100.0	122	3 US-08-437-642B-21	Sequence 21, Appl
30	24	100.0	122	5 PCT-US93-07832-21	Sequence 21, Appl
31	24	100.0	122	5 PCT-US93-08435-12	Sequence 12, Appl
32	24	100.0	122	5 PCT-US93-08435-14	Sequence 14, Appl
33	24	100.0	122	5 PCT-US93-08435-43	Sequence 43, Appl
34	24	100.0	123	2 US-08-428-197-38	Sequence 38, Appl
35	24	100.0	123	5 PCT-US93-10555-38	Sequence 38, Appl
36	24	100.0	124	4 US-08-983-607-47	Sequence 47, Appl
37	24	100.0	124	4 US-08-983-607-51	Sequence 51, Appl
38	24	100.0	125	1 US-08-478-039-99	Sequence 99, Appl
39	24	100.0	125	1 US-08-478-349A-99	Sequence 99, Appl
40	24	100.0	125	2 US-08-428-197-1	Sequence 1, Appl
41	24	100.0	125	5 PCT-US93-10555-1	Sequence 1, Appl
42	24	100.0	126	1 US-08-276-852-145	Sequence 145, App
43	24	100.0	126	1 US-08-899-575-145	Sequence 145, App
44	24	100.0	126	1 US-08-899-575-145	Sequence 145, App
45	24	100.0	126	5 PCT-US95-08743-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-07-977-696C-38
Sequence 38, Application US/07977696C
Patent No. 5792852
GENERAL INFORMATION:
APPLICANT: do Couto, Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 748-6868
TELEFAX: (510) 748-6688
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-977-696C-38
Query Match 100.0%, Score 24; DB 1; Length 5;
Best local Similarity 100.0%, Pred. No. 1, e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
Db 1 SYAMS 5

RESULT 2

US-08-129-930B-38
; Sequence 38, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; City: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-38

Query Match

Best Local Similarity 100.0%; Score 24; DB 1; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
Db 1 SYAMS 5

RESULT 3

US-08-134-346A-25
; Sequence 25, Application US/08134346A
; Patent No. 6281335
; GENERAL INFORMATION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Ceriani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ostrager, Chong & Flaherty
STREET: 300 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US

ZIP: 10022-7499

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/134,346A

FILING DATE: 08-OCT-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Onofrio, Dara L.

REGISTRATION NUMBER: 34,889

REFERENCE/DOCKET NUMBER: CLT 149, 608

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-826-5565

TELEFAX: 212-826-5909

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-134-346A-25

QY 1 SYAMS 5
|||||
Db 1 SYAMS 5

RESULT 4

US-08-976-288A-38
; Sequence 38, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; City: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,288A
; FILING DATE: No. 6315997ember 21, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: NO. 631597ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: P.A.
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-38

Query Match 100.0%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
DB 1 SYAMS 5

RESULT 5
PCT-US93-08435-16
Sequence 16, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid

TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-08435-16

Query Match 100.0%; Score 24; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
DB 1 SYAMS 5

RESULT 6
PCT-US93-08435-33
Sequence 33, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-08435-33

Query Match 100.0%; Score 24; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
DB 1 SYAMS 5

RESULT 7
US-08-208-886C-86
Sequence 86, Application US/0820886C

Patent No. 5597710
GENERAL INFORMATION:
APPLICANT: Dalle, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,886C
FILING DATE: March 10, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 2987
TELEFAX: 908 298 5388
INFORMATION FOR SEQ. ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-208-886C-86

Query Match 100.0%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
DB 6 SYAMS 10

RESULT 8
US-08-704-744-88
Sequence 88: Application US/08704744
Patent No. 5705134
GENERAL INFORMATION:
APPLICANT: Dalle, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2987
TELEFAX: (908) 298-5388
TELEX:
INFORMATION FOR SEQ. ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-744-88

Query Match 100.0%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
DB 6 SYAMS 10

RESULT 9
US-08-469-557-67
Sequence 67: Application US/08469557
Patent No. 5770403
GENERAL INFORMATION:
APPLICANT: Dalle, Barbara
APPLICANT: Le, Hung
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Nguyen, Hanh
APPLICANT: Tindall, Stephen
APPLICANT: Zavadny, Paul
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Humanized Monoclonal Antibodies
TITLE OF INVENTION: Against Human Interleukin-4
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,557
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,793
FILING DATE: August 16, 1994
APPLICATION NUMBER: PCT/US93/01301

;; FILING DATE: 19-FEB-1992
;; APPLICATION NUMBER: US 07/841,659
;; FILING DATE: 19-FEB-1992
;; APPLICATION NUMBER: US 07/782,784
;; FILING DATE: 24-OCT-1991
;; APPLICATION NUMBER: US 07/499,327
;; FILING DATE: 21-MAY-1990
;; APPLICATION NUMBER: PCT/US88/03631
;; FILING DATE: 21-OCT-1988
;; APPLICATION NUMBER: US 07/655,966
;; FILING DATE: 14-FEB-1991
;; APPLICATION NUMBER: US 07/113,623
;; FILING DATE: 26-OCT-1987
;; APPLICATION NUMBER: US 06/881,553
;; FILING DATE: 03-JUL-1986
;; APPLICATION NUMBER: US 06/843,958
;; FILING DATE: 25-MAR-1986
;; APPLICATION NUMBER: US 06/799,668
;; FILING DATE: 19-NOV-1985
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Foulke, Cynthia L.
;; REGISTRATION NUMBER: 32,364
;; REFERENCE/DOCKET NUMBER: 2409K7
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 908 298-2987
;; TELEFAX: 908 298-5388
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-469-557-67

Query Match 100.0%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
Db 6 SYAMS 10

RESULT 10
US-08-290-793B-67
; Sequence 67, Application US/08290793B
; Patent No. 5863537
; GENERAL INFORMATION:
; APPLICANT: Dalle, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; TITLE OF INVENTION: Against Human Interleukin-4
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1A
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/290,793B
;; FILING DATE: August 16, 1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/01301
;; FILING DATE: 19-FEB-1992
;; APPLICATION NUMBER: US 07/841,659
;; FILING DATE: 19-FEB-1992
;; APPLICATION NUMBER: US 07/782,784
;; FILING DATE: 24-OCT-1991
;; APPLICATION NUMBER: US 07/499,327
;; FILING DATE: 21-MAY-1990
;; APPLICATION NUMBER: PCT/US88/03631
;; FILING DATE: 21-OCT-1988
;; APPLICATION NUMBER: US 07/655,966
;; FILING DATE: 14-FEB-1991
;; APPLICATION NUMBER: US 07/113,623
;; FILING DATE: 26-OCT-1987
;; APPLICATION NUMBER: US 06/881,553
;; FILING DATE: 03-JUL-1986
;; APPLICATION NUMBER: US 06/843,958
;; FILING DATE: 25-MAR-1986
;; APPLICATION NUMBER: US 06/799,668
;; FILING DATE: 19-NOV-1985
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Foulke, Cynthia L.
;; REGISTRATION NUMBER: 32,364
;; REFERENCE/DOCKET NUMBER: 2409K7
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 908 298-2987
;; TELEFAX: 908 298-5388
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-290-793B-67

Query Match 100.0%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
Db 6 SYAMS 10

RESULT 11
US-08-765-179B-1
; Sequence 1, Application US/08765179B
; Patent No. 5854027
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; TITLE OF INVENTION: OF ANTIBODIES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,179B
; FILING DATE: 14-JAN-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-179B-1

Query Match 100.0%; Score 24; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
DB 31 SYAMS 35

RESULT 12
US-08-428-197-48
Sequence 48, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-197-48

Query Match 100.0%; Score 24; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
DB 31 SYAMS 35

RESULT 13
PCT-US93-10555-48
Sequence 48, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-10555-48

Query Match 100.0%; Score 24; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
DB 31 SYAMS 35

RESULT 14
US-08-273-146-65
Sequence 65, Application US/08273146
Patent No. 5855885
GENERAL INFORMATION:
APPLICANT: Smith, Rodger
APPLICANT: McCafferty, John
APPLICANT: Chiswell, David
APPLICANT: Darsley, Michael J.
APPLICANT: Fitzgerald, Kevin
APPLICANT: Keulen, John H.
APPLICANT: Martin, Mark T.
APPLICANT: Titmas, Richard C.
APPLICANT: Williams, Richard O.

TITLE OF INVENTION: The Isolation and Production of
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESS: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-273-146-65

Query Match 100.0%; Score 24; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
Db 15 SYAMS 19

RESULT 15
US-08-211-202-117
Sequence 117, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneus Jacobus Mattheus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6500
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-117

Query Match 100.0%; Score 24; DB 1; Length 110;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYAMS 5
|||||
Db 31 SYAMS 35

Search completed: June 21, 2002, 09:21:46
Job time: 409 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:41 ; Search time 109.39 Seconds
(without alignments)
14.933 Million cell updates/sec

Title: US-09-780-035-28_COPY_40_56
Perfect score: 86
Sequence: 1 A1SGSGSTYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : PIR71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	86	100.0	98	2	S26889 Ig heavy chain V r
2	86	100.0	99	2	S24259 Ig heavy chain V r
3	86	100.0	100	2	S24258 Ig heavy chain V r
4	86	100.0	101	2	S24257 Ig heavy chain V r
5	86	100.0	102	2	S24260 Ig heavy chain V r
6	86	100.0	104	2	S24255 Ig heavy chain V r
7	86	100.0	105	2	S24249 Ig heavy chain V r
8	86	100.0	106	2	S24256 Ig heavy chain V r
9	86	100.0	108	2	PH1648 Ig heavy chain V r
10	86	100.0	109	2	PH1649 Ig heavy chain V r
11	86	100.0	109	2	S24254 Ig heavy chain V r
12	86	100.0	109	2	S24253 Ig heavy chain V r
13	86	100.0	110	2	S24250 Ig heavy chain V r
14	86	100.0	112	2	PH1647 Ig heavy chain V r
15	86	100.0	113	2	S24247 Ig heavy chain V r
16	86	100.0	117	2	A45953 Ig heavy chain pre
17	86	100.0	118	2	S31121 Ig heavy chain - h
18	86	100.0	119	2	C36005 Ig heavy chain V r
19	86	100.0	119	2	D36005 Ig heavy chain V r
20	86	100.0	119	2	S31107 Ig heavy chain - h
21	86	100.0	119	2	S31108 Ig heavy chain - h
22	86	100.0	120	2	S48798 Ig heavy chain V r
23	86	100.0	121	2	S31113 Ig heavy chain - h
24	86	100.0	121	2	I35673 Ig heavy chain - h
25	86	100.0	123	2	S31114 Ig heavy chain - h
26	86	100.0	127	2	S38489 Ig heavy chain - h
27	86	100.0	138	2	S31666 Ig heavy chain V r
28	86	100.0	140	2	S31588 Ig heavy chain V r
29	86	100.0	160	2	S05271 Ig heavy chain pre

30	83	96.5	134	2	S31699 Ig heavy chain V r
31	83	96.5	140	2	S31686 Ig heavy chain V r
32	82	95.3	90	2	S24248 Ig heavy chain V r
33	82	95.3	117	1	H3HU26 Ig heavy chain pre
34	82	95.3	120	2	S36278 Ig heavy chain V r
35	81	94.2	111	2	S69911 Ig V-D-J region (R
36	81	94.2	113	2	S25571 Ig heavy chain V r
37	81	94.2	125	2	S72665 Ig V-D-J region (R
38	80	93.0	140	2	I47204 Ig heavy chain var
39	79	91.9	117	2	A34964 Ig heavy chain pre
40	78	90.7	98	2	S54856 Ig heavy chain V r
41	78	90.7	145	2	I47203 Ig heavy chain var
42	75	87.2	124	2	S20782 Ig heavy chain V r
43	74	86.0	120	2	E49580 Ig heavy chain V r
44	73	84.9	115	2	S09382 Ig heavy chain - C
45	73	84.9	117	2	B34964 Ig heavy chain pre

ALIGNMENTS

RESULT 1
S26889
Ig heavy chain V region (DP-47) - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26889
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A:Reference number: S26885; MUID:93021117
A:Accession: S26889
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12347; NID:G32914; PIDN:CAA78217.1; PID:G32915
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A1SGSGSTYYADSVKG 17
|||||
DB 50 A1SGSGSTYYADSVKG 66

RESULT 2
S24259
Ig heavy chain V region (VH26-DK1-JH4) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24259
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B
A:Reference number: S24247
A:Accession: S24259
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <STE>
A:Cross-references: EMBL:X67067; NID:G38391; PIDN:CAA47452.1; PID:G38392
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 A1SGSGGSTRYADSVKG 17
Db 35 A1SGSGGSTRYADSVKG 51

RESULT 3

S24258
Ig heavy chain V region (VH26-DXP1-JH4) - human
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24258
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24258
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-100 <STE>
A:Cross-references: EMBL:X67066; NID:g38389; PIDN:CAA47451.1; PID:g38390
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-86/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 A1SGSGGSTRYADSVKG 17
Db 38 A1SGSGGSTRYADSVKG 54

RESULT 4

S24257
Ig heavy chain V region (VH26-DXP1-JH4) - human
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24257
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24257
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <STE>
A:Cross-references: EMBL:X67065; NID:g38387; PIDN:CAA47450.1; PID:g38388
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-93/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 A1SGSGGSTRYADSVKG 17
Db 45 A1SGSGGSTRYADSVKG 61

RESULT 5

S24260
Ig heavy chain V region (VH26-DX1-JH4) - human
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S24260
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247
A:Accession: S24260
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <STE>
A:Cross-references: EMBL:X67068
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:5-87/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 A1SGSGGSTRYADSVKG 17
Db 39 A1SGSGGSTRYADSVKG 55

RESULT 6

S24255
Ig heavy chain V region (VH26-DLR5-JH4) - human
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S24255
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24255
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <STE>
A:Cross-references: EMBL:X67063
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:2-84/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 A1SGSGGSTRYADSVKG 17
Db 36 A1SGSGGSTRYADSVKG 52

RESULT 7

S24249
Ig heavy chain V region (VH26-DN1-DXP1-JH4) - human
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C:Accession: S24249
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
Submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24249
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-105 <STE>
A:Cross-references: EMBL:X67070
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY      1 AISGGGSTYYADSVKG 17
         |||||
Db      44 AISGGGSTYYADSVKG 60

```

RESULT
S24256

Ig heavy chain V region (VH26-DXp4-JH6) - human
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S24256
R/Stewart, A.K.; Huang, C.; Stollard, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A/Description: A single VH gene predominates in the rearranged and expressed human B cell repertoire.
A/Reference number: S24247
A/Accession: S24256
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-106 <StrE>
A/Cross-references: EMBL:X67064; NID:q38385; PIDN:CAA47449.1; PID:q38386
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;4-86/Domain: immunoglobulin homology <IMM>

Query Match	100.0%;	Score 86;	DB 2;	Length 106;
Best Local Similarity	100.0%;	Pred. No. 3.9e-06;		
Matches 17; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

```
QY      1 AISGGGSTYYADSVKG 17
          |||||
Db     38 AISGGGSTYYADSVKG 54
```

RESULT

Ig heavy chain V region (clone 2B8) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: PH1648
 R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
 A:Reference number: PH1642; MUID:53301610
 A:Accession: PH1648
 A:Molecule type: mRNA
 A:Residues: 1-108 <HTL>
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match	100.0%;	Score 86;	DB 2;	Length 108;
Best Local Similarity	100.0%;	Pred. NO. 4e-06;		
Matches 17; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

```
QY      1 AISGGGSTYYADSVKG 17
         |||
Db      42 AISGGGSTYYADSVKG 58
```

RESULTS

I9 heavy chain V region (clone 2E7) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: PH1649
 R:Hallson, J. L.; Karr, N. S.; Opplinger, I. R.; Mannik, M.; Sasso, E. H.
 J. Exp. Med. 178, 333-336, 1993
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
 #:Reference number: PH1642; MUID:93301610
 #:Accession: PH1649

A: Molecule type: mRNA
A: Residues: 1-109 <HTL>
A: Experimental source: B cell
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin
E: 7-90/Domain: immunoglobulin homology <IM>

Query Match	100.0%;	Score 86;	DB 2;	Length 109;
Best Local Similarity	100.0%;	Pred. No. 4e-06;		
Matches 17; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
QY      1 AISGSGGSTYYADSVKG 17
          |||||
Db      42 AISGSGGSTYYADSVKG 56
```

RESULT 11
S24254

Ig heavy chain V region (VH4b-DXP2-JH4) - human
 C:Species: Homo sapiens (man)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S24254
 R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
 submitted to the EMBL Data library, June 1992
 A:Description: A single VH gene predominates in the rearranged and expressed human B
 A:Reference number: S24247
 A:Accession: S24254
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-109 <STE>
 A:Cross-references: EMBL:X67062
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 E:15-97/Domain: immunoglobulin homology <IMM>

Query Match	100.0%;	Score 86;	DB 2;	Length 109;
Best Local Similarity	100.0%;	Pred. No. 4e-06;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```
QY 1 AISGSGSTYYADSVKG 17
    |||||
Db 49 AISGSGSTYYADSVKG 65
```

RESULT	12
S24253	

Ig heavy chain V region (VH26-DLR4-JH6) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24253
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B
A:Reference number: S24247
A:Accession: S24253
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <STE>
A:Cisot-references: EMBL:X67061
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
E:12-94/Domain: immunoglobulin homology <IMM>

Query Match	100.0%;	Score 86;	DB 2;	Length 109;
Best Local Similarity	100.0%;	Pred. No. 4e-06;		
Matches 17; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	AISGSGGTTYADSVKG	17
Db	46	AISGSGGTTYADSVKG	62

RESULT 13

S24250

Ig heavy chain V region (VH26-DNI-JH4) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S24250

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

Submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24250

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-110 <STE>

A:Cross-references: EMBL:X67071

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 4e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AISGSGSTYYADSVKG 17

Db 49 AISGSGSTYYADSVKG 65

RESULT 14

PH1647

Ig heavy chain V region (clone 2D10) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C:Accession: PH1647

R:Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc

A:Reference number: PH1642; MUID:93301610

A:Accession: PH1647

A:Molecule type: mRNA

A:Residues: 1-112 <HIL>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4.1e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AISGSGSTYYADSVKG 17

Db 42 AISGSGSTYYADSVKG 58

RESULT 15

S24247

Ig heavy chain V region (VH26-DLR2-JH3) - human

C:Species: Homo sapiens (man)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S24247

R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.

Submitted to the EMBL Data Library, June 1992

A:Description: A single VH gene predominates in the rearranged and expressed human B cell

A:Reference number: S24247

A:Accession: S24247

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-113 <STE>

A:Cross-references: EMBL:X67060; NID:938377; PIDN:CAA47445.1; PID:938378
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AISGSGSTYYADSVKG 17

Db 49 AISGSGSTYYADSVKG 65

Search completed: June 21, 2002, 09:23:41
 Job time: 494 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:48:16 ; Search time 52.75 Seconds

(Without alignments)
12.478 Million cell updates/sec

Title: US-09-780-035-28_COPY_40_56
Perfect score: 86
Sequence: 1 A1SGSGGSTRYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	95.3	117	1	HV3C_HUMAN
2	68	79.1	116	1	HV05_CARAU
3	66	76.7	117	1	HV53_MOUSE
4	64	74.4	117	1	HV54_MOUSE
5	64	74.4	117	1	HV55_MOUSE
6	63	73.3	97	1	HV56_MOUSE
7	63	73.3	114	1	HV3B_HUMAN
8	63	73.3	122	1	HV3A_HUMAN
9	61	70.9	113	1	HV3E_HUMAN
10	56	65.1	119	1	HV3L_HUMAN
11	55	64.0	117	1	HV02_CANFA
12	55	64.0	120	1	HV3E_HUMAN
13	55	64.0	120	1	HV3U_HUMAN
14	54	62.8	98	1	HV57_MOUSE
15	53	61.6	117	1	HV59_MOUSE
16	51	59.3	117	1	HV58_MOUSE
17	50	58.1	121	1	HV3J_HUMAN
18	50	58.1	122	1	HV3G_HUMAN
19	47	54.7	111	1	HV35_MOUSE
20	46.5	54.1	275	1	RR40_HUMAN
21	46.5	54.1	694	1	PNKL_NPVAC
22	45	52.3	356	1	K523_HAEIN
23	44.5	51.7	136	1	HV16_MOUSE
24	44	51.2	115	1	HV3D_HUMAN
25	44	51.2	122	1	HV3H_HUMAN
26	43	50.0	117	1	HV1B_HUMAN
27	43	50.0	126	1	HV3K_HUMAN
28	43	50.0	314	1	SERR_HAEIN
29	43	50.0	579	1	GPC2_RAT
30	43	50.0	790	1	YDDB_ECOLI
31	42	48.8	116	1	HV1A_RABIT
32	42	48.8	383	1	MANA_STRLI
33	42	48.8	473	1	PGPD_BUCAP

34	41	47.7	319	1	KHSE_AERPE
35	41	47.7	376	1	GUNK_FUSOX
36	41	47.7	423	1	SNX4_YEAST
37	40	46.5	113	1	HV27_MOUSE
38	40	46.5	113	1	HV28_MOUSE
39	40	46.5	113	1	HV29_MOUSE
40	40	46.5	113	1	HV30_MOUSE
41	40	46.5	115	1	HV32_MOUSE
42	40	46.5	115	1	HV02_XENLA
43	40	46.5	135	1	YPOL_ACICA
44	40	46.5	204	1	ACOA_ALCEU
45	40	46.5	332	1	

ALIGNMENTS

RESULT 1
HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE I9 heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matlyssens G., Rabbits T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin heavy chain variable region."
RT Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).

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CC EMBL: J00236; AAA53516.1; -
DR EMBL: M35415; AAA58735.1; -
DR PIR: A02047; H3H026.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR003596; Iq_V.
DR Pfam: PF00047; Iq_1.
DR SMART: SM00406; IqV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 95.3%; Score 82; DB 1; Length 117;
Best Local Similarity 94.1%; Pred. No. 2,1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 A1SGSGGSTRYADSVKG 17
DB 69 A1SGSGGSTRYADSVKG 85

RESULT 2
HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5A precursor.
 OS Carassius auratus (Goldfish).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 CC Cypriniformes; Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88144476; PubMed=3125551;
 RA Wilson M.R., Middleton D., Marr G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure
 RT and family relationships of two genes and a pseudogene in a teleost
 RT fish."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 DR PIR: B28966; B28966.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig, 1.
 DR SMART: SM00406; IgV, 1.
 KW Immunoglobulin V region; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DISULFID 41 114 BY SIMILARITY.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 79.1%; Score 68; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SGGSTYYADSVKG 17
 DB 72 SGGSTYYADSVKG 84

RESULT 3
 HV53_MOUSE STANDARD; PRT; 117 AA.
 AC P18524;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region RF precursor.
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BALB/CJ;
 RA MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JTO503; HVMSR.
 DR HSSP: P01810; 2FBJ.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig, 1.
 DR SMART: SM00406; IgV, 1.
 KW Immunoglobulin V region; Hybridoma; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.

FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 76.7%; Score 66; DB 1; Length 117;
 Best Local Similarity 70.6%; Pred. No. 0.00077;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AINSGGSTYYADSVKG 17
 DB 69 AINSGGSTYYADSVKG 85

RESULT 4
 HV54_MOUSE STANDARD; PRT; 117 AA.
 AC P18525;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 5-84 precursor.
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BALB/CJ;
 RA MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: JTO505; HVMS84.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig, 1.
 DR SMART: SM00406; IgV, 1.
 KW Immunoglobulin V region; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12872 MW; 234055CE6A469861 CRC64;

Query Match 74.4%; Score 64; DB 1; Length 117;
 Best Local Similarity 75.0%; Pred. No. 0.0016;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISNGGSTYYADSVKG 17
 DB 70 ISNGGSTYYADSVKG 85

RESULT 5
 HV55_MOUSE STANDARD; PRT; 117 AA.
 AC P18526;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:18 ; Search time 194.32 Seconds

(without alignments)
15.134 Million cell updates/sec

Title: US-09-780-035-28_COPY_40_56

Perfect score: 86

Sequence: 1 AISSGGSGSTYYADSVKG 17

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	597	4 Q96BB9	Q96BB9 homo sapien
2	78	90.7	121	4 Q9UL71	Q9UL71 homo sapien
3	66	76.7	118	4 Q9UL72	Q9UL72 homo sapien
4	62	72.1	479	11 Q91WP5	Q91WP5 mus musculu
5	58	67.4	112	4 Q9HCC1	Q9HCC1 homo sapien
6	57	66.3	122	4 Q9UL84	Q9UL84 homo sapien
7	57	66.3	486	11 Q91Z07	Q91Z07 mus musculu
8	55	64.0	119	11 Q920E7	Q920E7 mus musculu
9	54	62.8	116	4 Q9UL93	Q9UL93 homo sapien
10	52	60.5	112	4 Q9HGP3	Q9HGP3 homo sapien
11	52	60.5	437	11 Q9R1A4	Q9R1A4 mus musculu
12	51	59.3	416	4 Q9NPP6	Q9NPP6 homo sapien
13	51	59.3	480	11 Q91XE1	Q91XE1 mus musculu
14	51	59.3	487	11 Q99KA4	Q99KA4 mus musculu
15	49	57.0	104	4 Q9UL87	Q9UL87 homo sapien
16	49	57.0	113	4 Q9UL90	Q9UL90 homo sapien

17	47	54.7	147	4 Q9Y509	Q9Y509 homo sapien
18	47	54.7	295	10 Q9ZSR4	Q9ZSR4 mesembryant
19	47	54.7	1284	5 Q9Y562	Q9Y562 drosophila
20	46.5	54.1	79	4 Q9NYS3	Q9NYS3 homo sapien
21	46.5	54.1	473	11 Q91Z05	Q91Z05 mus musculu
22	46	53.5	95	4 Q9ULB6	Q9ULB6 homo sapien
23	46	53.5	430	5 Q95UF6	Q95UF6 caenorhabdi
24	46	53.5	447	5 Q9GVG3	Q9GVG3 caenorhabdi
25	45	52.3	956	2 Q9XAP9	Q9XAP9 ehllichia c
26	44	51.2	118	4 Q9UL91	Q9UL91 homo sapien
27	44	51.2	238	16 Q50817	Q50817 borrelia bu
28	44	51.2	1265	2 Q9FPA0	Q9FPA0 xanthomonas
29	43	50.0	124	4 Q9UL92	Q9UL92 homo sapien
30	43	50.0	129	2 Q60111	Q60111 yersinia ps
31	43	50.0	147	13 Q98UB9	Q98UB9 notochenia
32	43	50.0	147	13 Q98UB8	Q98UB8 notochenia
33	43	50.0	185	16 Q32786	Q32786 lactococcus
34	43	50.0	185	16 Q9CB10	Q9CB10 lactococcus
35	43	50.0	309	10 Q65213	Q65213 volvox cart
36	43	50.0	326	2 Q46142	Q46142 clostridium
37	43	50.0	371	10 Q9SXC6	Q9SXC6 oryza sativ
38	43	50.0	386	2 Q93JX2	Q93JX2 pseudomonas
39	43	50.0	474	10 Q04036	Q04036 arabidopsis
40	43	50.0	496	10 Q65799	Q65799 arabidopsis
41	43	50.0	536	2 Q93JK8	Q93JK8 streptomyc
42	43	50.0	654	5 Q95Y06	Q95Y06 leishmania
43	43	50.0	1251	6 Q28224	Q28224 cercopithec
44	42.5	49.4	243	11 Q9CVM2	Q9CVM2 mus musculu
45	42	48.8	124	5 Q95TEL	Q95TEL drosophila

ALIGNMENTS

RESULT	ID	Q96BB9	PRELIMINARY;	PRT;	597 AA.
AC	Q96BB9;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	HYPOTHETICAL 65.0 KDA PROTEIN.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
NCBI	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PRIMARY B-CELLS FROM TONSILS;				
RA	Strausberg R.;				
RL	Submitted (OCF-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC015760; AAH15760.1; -				
KW	HYPOTHETICAL protein.				
SQ	SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;				

Query Match	100.0%;	Score 86;	DB 4;	Length 597;
Best Local Similarity	100.0%;	Pred. No. 2.3e-05;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 AISSGGSGSTYYADSVKG 17			
DB	69 AISSGGSGSTYYADSVKG 85			
RESULT	2			
Q9UL71	PRELIMINARY;	PRT;	121 AA.	
AC	Q9UL71;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION			

DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035043; AAD56279.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1 1
FT SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 90.7%; Score 78; DB 4; Length 121;
Best Local Similarity 93.8%; Pred. No. 6.6e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ISGSGSTYADSVKG 17
DB 51 ISGSGSTYADSVKG 66

RESULT 3
ID 09UL72 PRELIMINARY; PRT; 118 AA.
AC 09UL72;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035042; AAD56278.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1 1
FT SEQUENCE 118 AA; 12872 MW; BAD1A5944B2D5CCA CRC64;

Query Match 76.7%; Score 66; DB 4; Length 118;
Best Local Similarity 70.6%; Pred. No. 0.0053;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 AISGSGSTYADSVKG 17
DB 49 SVTSGSGSTYADSVKG 65

RESULT 4
ID 091WP5 PRELIMINARY; PRT; 479 AA.
AC 091WP5;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE HYPOETHERICAL 51.6 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013656; AAH13656.1; -.
DR Hypothetical protein.
KW Hypothetical protein.
FT SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 72.1%; Score 62; DB 11; Length 479;
Best Local Similarity 58.8%; Pred. No. 0.12;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 AISGSGSTYADSVKG 17
DB 69 AINSGGNTYSDPMKG 85

RESULT 5
ID 09HCC1 PRELIMINARY; PRT; 112 AA.
AC 09HCC1;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE SINGLE CHAIN FV (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme: Isolation from a
human synthetic phage display library and characterization."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB049915; BAB16829.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; Ig_like; 1.
FT NON_TER 1 1
FT SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 67.4%; Score 58; DB 4; Length 112;
Best Local Similarity 75.0%; Pred. No. 0.093;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 ISGSGSTYADSVKG 17
DB 51 INMNGSTYADSVKG 66

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:15 ; Search time 245.49 Seconds
(without alignments)
7.692 Million cell updates/sec

Title: US-09-780-035-28_COPY_40_56
Perfect score: 86
Sequence: 1 AIGSGGSTRYADSVK 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
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19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	17	18	AAW16651
2	86	100.0	17	21	AAAY95213
3	86	100.0	17	22	AAAG5311
4	86	100.0	56	20	AAAY02512
5	86	100.0	56	20	AAAY02516
6	86	100.0	56	20	AAAY02517
7	86	100.0	56	20	AAAY02518
8	86	100.0	56	20	AAAY02520
9	86	100.0	56	20	AAAY02522
10	86	100.0	56	20	AAAY02524
11	86	100.0	56	20	AAAY02525

12	86	100.0	56	20	AAAY02496	Clone selected aft
13	86	100.0	56	20	AAAY02497	Clone selected aft
14	86	100.0	56	20	AAAY02504	Clone selected aft
15	86	100.0	56	20	AAAY02505	Clone selected aft
16	86	100.0	56	20	AAAY02508	Clone selected aft
17	86	100.0	56	20	AAAY02509	Clone selected aft
18	86	100.0	56	20	AAAY02484	Clone selected aft
19	86	100.0	56	20	AAAY02485	Clone selected aft
20	86	100.0	56	20	AAAY02486	Clone selected aft
21	86	100.0	56	20	AAAY02487	Clone selected aft
22	86	100.0	56	20	AAAY02488	Clone selected aft
23	86	100.0	56	20	AAAY02493	Clone selected aft
24	86	100.0	56	20	AAAY02494	Clone selected aft
25	86	100.0	56	20	AAAY02495	Clone selected aft
26	86	100.0	56	20	AAAY02474	Clone selected aft
27	86	100.0	56	20	AAAY02478	Clone selected aft
28	86	100.0	98	21	AAAB40093	Anti-hi112 antibod
29	86	100.0	98	21	AAAY50972	Human FVIII antibo
30	86	100.0	98	21	AAE12710	Antibody variable
31	86	100.0	108	22	AAAG65318	Anti-IL-18 antibod
32	86	100.0	110	18	AAW41017	Anti-glutathione a
33	86	100.0	112	21	AAAY95183	Anti-platelet glyc
34	86	100.0	112	21	AAAY95184	Anti-platelet glyc
35	86	100.0	113	19	AAW47179	Variable heavy (VH
36	86	100.0	115	21	AAAY95210	Anti-platelet glyc
37	86	100.0	115	21	AAAY95211	Anti-platelet glyc
38	86	100.0	115	22	AAU02581	Anti-adipocyte mon
39	86	100.0	116	18	AAW13529	Anti-melanoma anti
40	86	100.0	116	22	AAE07017	Human heavy chain
41	86	100.0	117	16	AAW65315	Human immunoglobul
42	86	100.0	117	18	AAW13532	Anti-melanoma anti
43	86	100.0	117	22	AAE07020	Human heavy chain
44	86	100.0	118	18	AAW19878	CRA-specific antib
45	86	100.0	118	22	AAAG65354	Anti-IL-18 antibod

ALIGNMENTS

RESULT 1
ID AAW16651 standard; Peptide: 17 AA.
AC AAW16651:
DT 29-DAN-1998 (first entry)
DE Anti-cancer specific antigen Mab heavy chain CDR2.
XX Heavy chain; variable region; cancer specific antigen; human;
KW monoclonal antibody; hmb; diagnosis; cancer; immunotherapy;
KW purification; complementarity determining region 2; CDR2.
XX
OS Homo sapiens.
PN JP09098786-A.
PD 15-APR-1997.
PF 06-OCT-1995; 95JP-0284400.
PR 06-OCT-1995; 95JP-0284400.
XX
XX (MOMI) MORINAGA & CO LTD.
PA (SHKJ) SHINGIUTSU JIGYODAN.
XX
DR WPI: 1997-275445/25.
DR N-PSDB; AAT66783.
PT CDNA encoding human monoclonal antibody - useful in medicine, or to
PT purify cancer specific antigen
XX
PS Claim 9; Fig 12; 7p; Japanese.

XX CC The present sequence is the heavy chain complementarity
 CC determining region 2 of an anti-cancer specific antigen human
 CC monoclonal antibody (hMab). The hMab can be used in medicine, e.g.
 CC clinical diagnosis of cancer or immunotherapy, or to purify cancer
 CC specific antigen. The industrial scale production of large amounts
 CC of the hMab is made feasible by genetic engineering using the hMab
 CC cDNA.

XX SO Sequence 17 AA:

Query Match 100.0%; Score 86; DB 18; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AISGSGSTYYADSVKG 17
 |||||
 DB 1 aissgsstyadsvkg 17

RESULT 2
 ID AAY95213 standard; Peptide; 17 AA.
 XX AAY95213;
 AC AAY95213;
 XX 29-AUG-2000 (first entry)
 DT Anti-platelet glycoprotein Ib human HIB-3 VH CDR2.
 DE Variable heavy chain; single chain antibody; scFv; human; HIB-3;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic; CDR2;
 KW complementarity determining region.
 XX Homo sapiens.
 OS WO200026667-A1.
 PN 11-MAY-2000.
 XX 29-OCT-1999; 99WO-US25495.
 PF 30-OCT-1998; 98US-0106275.
 XX (MILLER) MILLER J L.
 PA Miller JL;
 PI WPI; 2000-365744/31.
 DR Isolated nucleic acid molecule encoding anti-human platelet
 PT glycoprotein Ib alpha molecule useful for producing antibodies which
 PT inhibit platelet aggregation -
 XX Claim 15; Fig 7; 89pp; English.

XX CC The present sequence is that of complementarity determining region
 CC 2 (CDR2) of the heavy chain variable region (VH) of human
 CC single chain antibody (scFv) HIB-3 (see AAY95213), which is directed
 CC against platelet glycoprotein Ib (GPIb). The HIB series of scFv
 CC was isolated from a human synthetic VH and VL scFv library on the
 CC basis of their binding to platelet GPIb. Whether displayed as
 CC surface proteins on a phagemid or secreted as free scFv by
 CC *Escherichia coli*, the HIB scFv clones are capable of inhibiting
 CC von Willebrand factor-dependent aggregation of platelets. The scFv
 CC are composed of native human protein sequences and are therefore
 CC attractive potential reagents for therapeutic purposes. They
 CC provide a new class of antithrombotic agents, useful for the
 CC prevention of platelet-dependent thrombi in diseased arteries,
 CC bypass grafts, dialysis etc., and can also be used as diagnostic
 CC reagents. Methods of inhibiting aggregation of platelets, of

XX CC binding human platelet GPIb alpha and of selecting a VH or VL
 CC region of an antibody that inhibits platelet aggregation are
 CC claimed. Fragments of the scFv VH or VL chain, including CDR
 CC fragments, are also claimed.

XX SO Sequence 17 AA:

Query Match 100.0%; Score 86; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AISGSGSTYYADSVKG 17
 |||||
 DB 1 aissgsstyadsvkg 17

RESULT 3
 ID AAG65311 standard; protein; 17 AA.
 XX AAG65311;
 AC AAG65311;
 XX 30-NOV-2001 (first entry)
 DT Anti-IL-18 antibody LIT28 heavy chain CDR2 fragment.
 DE IL-18; interleukin-18; human; antibody; antineumatic; cerebroprotective;
 KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiact;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LIT28.
 XX Homo sapiens.
 OS WO200158956-A2.
 PN 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US04170.
 PF 10-FEB-2000; 2000US-0181608.
 XX (BADI) BASF AG.
 PA Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Leonard SN;
 XX WPI; 2001-550020/61.
 DR Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX Claim 32; Page 41; 91pp; English.

XX CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrently, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LIT28
 CC heavy chain CDR2 fragment.

Sequence 17 AA:

Query Match 100.0%; Score 86; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AISGSGSTYYADSVKG 17
|
Db 1 aissgsgstyadsvkg 17

RESULT 4

AA02512
ID AAY02512 standard; Protein; 56 AA.

AC AAY02512;

DT 15-JUL-1999 (first entry)

DE Clone selected after panning a NNK library of the invention.

KW Screening; functional polypeptide; ligand; non-functional;

enrichment; single chain antibody; ScFv.

OS Synthetic.

PN WO9920749-A1.

PD 29-APR-1999.

PF 20-OCT-1998; 98WO-GB03135.

PR 21-NOV-1997; 97US-0066729.

PR 20-OCT-1997; 97GB-0022131.

PR 13-NOV-1997; 97US-0065428.

XX (MEDI-) MEDICAL RES COUNCIL.

PI Tomlinson I, Winter G;

DR WPI; 1999-288302/24.

PT Screening for functional polypeptides which bind a ligand

PS Example 3; Fig 4; 67pp; English.

XX The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in
CC diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525
CC represent clones selected after panning primary and somatic NNK
CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
CC NIP-BSA and hen egg lysozyme).

Sequence 56 AA:

Query Match 100.0%; Score 86; DB 20; Length 56;

Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AISGSGSTYYADSVKG 17
|
Db 6 aissgsgstyadsvkg 22

RESULT 5

AA02516
ID AAY02516 standard; Protein; 56 AA.

AC AAY02516;

DT 15-JUL-1999 (first entry)

DE Clone selected after panning a NNK library of the invention.

KW Screening; functional polypeptide; ligand; non-functional;

enrichment; single chain antibody; ScFv.

OS Synthetic.

PN WO9920749-A1.

PD 29-APR-1999.

PF 20-OCT-1998; 98WO-GB03135.

PR 21-NOV-1997; 97US-0066729.

PR 20-OCT-1997; 97GB-0022131.

PR 13-NOV-1997; 97US-0065428.

XX (MEDI-) MEDICAL RES COUNCIL.

PI Tomlinson I, Winter G;

DR WPI; 1999-288302/24.

PT Screening for functional polypeptides which bind a ligand

PS Example 3; Fig 4; 67pp; English.

XX The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in
CC diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525
CC represent clones selected after panning primary and somatic NNK
CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
CC NIP-BSA and hen egg lysozyme).

Sequence 56 AA:

Query Match 100.0%; Score 86; DB 20; Length 56;

Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AISGSGSTYYADSVKG 17
|
Db 6 aissgsgstyadsvkg 22

RESULT 6

AA02517
ID AAY02517 standard; Protein; 56 AA.

AC AAY02517;

DT 15-JUL-1999 (first entry)

XX

```

DE Clone selected after panning a NNK library of the invention.
XX
XX Screening; functional polypeptide; ligand; non-functional;
KW enrichment; single chain antibody; ScFv.
XX
XX Synthetic.
OS
PN WO9920749-A1.
PD
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-GB03135.
XX
XX 21-NOV-1997; 97US-0066729.
XX 20-OCT-1997; 97GB-0022131.
XX 13-NOV-1997; 97US-0065428.
XX
XX (MEDT-) MEDICAL RES COUNCIL.
XX
XX Tomlinson I, Winter G;
XX
XX WPI; 1999-288302/24.
XX
XX Screening for functional polypeptides which bind a ligand
PT
XX Example 3; Fig 4; 67pp; English.
PS
XX The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in
CC diagnostic, prophylactic and therapeutic procedures. AAY02473-102525
CC represent clones selected after panning primary and somatic NNK
CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
CC NIP-BSA and hen egg lysozyme).
XX
XX Sequence 56 AA:
SQ
Query Match 100.0%; Score 86; DB 20; Length 56;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AISGSGSTYYADSVKG 17
| | | | | | | | | | | | | | | | |
DB 6 aISGsgstlyadsvkg 22
RESULT 7
ID AAY02518
AY02518 standard; Protein: 56 AA.
XX
XX AAY02518;
XX
XX 15-JUL-1999 (first entry)
XX
XX Clone selected after panning a NNK library of the invention.
XX Screening; functional polypeptide; ligand; non-functional;
KW enrichment; single chain antibody; ScFv.
XX
XX Synthetic.
XX
XX WO9920749-A1.
XX
XX 29-APR-1999.
XX

```

PF		20-OCT-1998;	98WO-GB03135.	
XX				
PR	XX	21-NOV-1997;	97US-0066729.	
PR	XX	20-OCT-1997;	97GB-0022131.	
PR	XX	13-NOV-1997;	97US-0065428.	
PA	XX	(MEDI-) MEDICAL RES COUNCIL.		
PI	XX	Tomlinson I, Winter G;		
DR	XX	WPI; 1999-288302/24.		
PT	XX	Screening for functional polypeptides which bind a ligand		
PS	XX	Example 3; Fig 4; 67pp; English.		
CC	XX	The specification describes a method for screening for functional		
CC	XX	polypeptides which bind a ligand. The method comprises contacting a		
CC	XX	repertoire of polypeptides with a generic ligand, and then screening		
CC	XX	selected functional polypeptides with a target ligand. The method		
CC	XX	permits the removal from a chosen repertoire of polypeptides, those		
CC	XX	which are non-functional, e.g. as a result of the introduction of		
CC	XX	frame-shift mutations, stop codons, folding mutants or expression		
CC	XX	mutants which would be or are incapable of binding to any target		
CC	XX	ligand. The method also permits the enrichment of a chosen repertoire		
CC	XX	of polypeptides for those polypeptides which are functional, well folded		
CC	XX	and highly expressed. The polypeptides obtained can be used in		
CC	XX	diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525		
CC	XX	represent clones selected after panning primary and somatic NK		
CC	XX	libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,		
CC	XX	NIF-BSA and hen egg lysozyme).		
SQ	XX	Sequence 56 AA;		
OY		Query Match 100.0%; Score 86; DB 20; Length 56;		
		Best Local Similarity 100.0%; Pred. No. 7e-06;		
		Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
DG		1 AIGSGGSSTYYADSVKG 17		
DB		6 AISGSGSSTYYADSVK 22		
RESULT	8			
ID	AAY02520	standard; Protein; 56 AA.		
AC	AAY02520;			
DT	15-JUL-1999	(first entry)		
DE		Clone selected after panning a NKK library of the invention.		
KW		Screening; functional polypeptide; ligand; non-functional;		
XX		enrichment; single chain antibody; ScFv.		
OS		Synthetic.		
PN	M09920749-AI.			
PD	29-APR-1999.			
PE	20-OCT-1998;	98WO-GB03135.		
PR	21-NOV-1997;	97US-0066729.		
PR	20-OCT-1997;	97GB-0022131.		
PR	13-NOV-1997;	97US-0065428.		
RA	(MEDI-) MEDICAL RES COUNCIL.			
TI	Tomlinson I, Winter G;			

CC Libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
 CC NIP-BSA and hen egg lysozyme).
 XX
 SQ Sequence 56 AA;

Query Match 100.0%; Score 86; DB 20; Length 56;
 Best Local Similarity 100.0%; Pred. No. 7e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AISGSGSTYYADSVKG 17
 |||||
 Db 6 aissgsgstyadsvkg 22

RESULT 11

AAI02525
 ID AAY02525 standard; Protein; 56 AA.

XX
 AC AAY02525;

XX
 DT 15-JUL-1999 (first entry)

XX
 DE Clone selected after panning a NNK library of the invention.

XX
 KW Screening; functional polypeptide; ligand; non-functional;

KW enrichment; single chain antibody; ScFv.

XX
 OS Synthetic.

XX
 PN WO9920749-A1.

XX
 PD 29-APR-1999.

XX
 PF 20-OCT-1998; 98WO-GB03135.

XX
 PR 21-NOV-1997; 97US-0066729.

XX
 PR 20-OCT-1997; 97GB-0022131.

XX
 PR 13-NOV-1997; 97US-0065428.

XX
 PA (MEDI-) MEDICAL RES COUNCIL.

XX
 PT Tomlinson I, Winter G;

XX
 DR WPI; 1999-288302/24.

XX
 PS Screening for functional polypeptides which bind a ligand

XX
 PS Example 3; Fig 4; 67pp; English.

XX The specification describes a method for screening for functional
 CC polypeptides which bind a ligand. The method comprises contacting a
 CC repertoire of polypeptides with a generic ligand, and then screening
 CC selected functional polypeptides with a target ligand. The method
 CC permits the removal from a chosen repertoire of polypeptides, those
 CC which are non-functional, e.g. as a result of the introduction of
 CC frame-shift mutations, stop codons, folding mutants or expression
 CC mutants which would be or are incapable of binding to any target
 CC ligand. The method also permits the enrichment of a chosen repertoire
 CC of polypeptides for those polypeptides which are functional, well folded
 CC and highly expressed. The polypeptides obtained can be used in
 CC diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525
 CC represent clones selected after panning primary and somatic NNK
 CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
 CC NIP-BSA and hen egg lysozyme).

XX
 SQ Sequence 56 AA;

Query Match 100.0%; Score 86; DB 20; Length 56;
 Best Local Similarity 100.0%; Pred. No. 7e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AISGSGSTYYADSVKG 17
 |||||
 Db 6 aissgsgstyadsvkg 22

RESULT 12

AAI02496
 ID AAY02496 standard; Protein; 56 AA.

XX
 AC AAY02496;

XX
 DT 15-JUL-1999 (first entry)

XX
 DE Clone selected after panning a NNK library of the invention.

XX
 KW Screening; functional polypeptide; ligand; non-functional;

KW enrichment; single chain antibody; ScFv.

XX
 OS Synthetic.

XX
 PN WO9920749-A1.

XX
 PD 29-APR-1999.

XX
 PF 20-OCT-1998; 98WO-GB03135.

XX
 PR 21-NOV-1997; 97US-0066729.

XX
 PR 20-OCT-1997; 97GB-0022131.

XX
 PR 13-NOV-1997; 97US-0065428.

XX
 PA (MEDI-) MEDICAL RES COUNCIL.

XX
 PT Tomlinson I, Winter G;

XX
 DR WPI; 1999-288302/24.

XX
 PS Screening for functional polypeptides which bind a ligand

XX
 PS Example 3; Fig 4; 67pp; English.

XX The specification describes a method for screening for functional
 CC polypeptides which bind a ligand. The method comprises contacting a
 CC repertoire of polypeptides with a generic ligand, and then screening
 CC selected functional polypeptides with a target ligand. The method
 CC permits the removal from a chosen repertoire of polypeptides, those
 CC which are non-functional, e.g. as a result of the introduction of
 CC frame-shift mutations, stop codons, folding mutants or expression
 CC mutants which would be or are incapable of binding to any target
 CC ligand. The method also permits the enrichment of a chosen repertoire
 CC of polypeptides for those polypeptides which are functional, well folded
 CC and highly expressed. The polypeptides obtained can be used in
 CC diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525
 CC represent clones selected after panning primary and somatic NNK
 CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
 CC NIP-BSA and hen egg lysozyme).

XX
 SQ Sequence 56 AA;

Query Match 100.0%; Score 86; DB 20; Length 56;
 Best Local Similarity 100.0%; Pred. No. 7e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AISGSGSTYYADSVKG 17
 |||||
 Db 6 aissgsgstyadsvkg 22

RESULT 13

AAI02497
 ID AAY02497 standard; Protein; 56 AA.

XX
 AC AAY02497;


```

XX 15-JUL-1999 (first entry)
DT
XX Clone selected after panning a NNK library of the invention.
DE
XX Screening; functional polypeptide; ligand; non-functional;
RW enrichment; single chain antibody; scFv.
XX
XX Synthetic.
OS
XX WO9920749-A1.
PN
XX 29-APR-1999.
PD
XX 20-OCT-1998; 98WO-GB03135.
PE
XX 21-NOV-1997; 97US-0066729.
PR 20-OCT-1997; 97GB-0022131.
PR 13-NOV-1997; 97US-0065428.
XX
XX (MEDT-) MEDICAL RES COUNCIL.
PA
XX Tomlinson I, Winter G;
PI
XX WPI, 1999-288302/24.
DR
XX
XX Screening for functional polypeptides which bind a ligand
PT
XX
XX Example 3; Fig 4; 67pp; English.
PS
XX
XX The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in
CC diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525
CC represent clones selected after panning primary and somatic NNK
CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
CC NIP-BSA and hen egg lysozyme).
CC
XX
XX Sequence 56 AA;
SQ

```

```

Query Match 100.0%; Score 86; DB 20; Length 56;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 AISGSGSTYYADSVKG 17
   |||||||
Db 6 aisgsgstyadsvkg 22

```

```

RESULT 14
AAY02504
ID AAY02504 standard; Protein; 56 AA.
XX
XX AAY02504;
AC
XX
XX 15-JUL-1999 (first entry)
DT
XX
XX Clone selected after panning a NNK library of the invention.
DE
XX Screening; functional polypeptide; ligand; non-functional;
RW enrichment; single chain antibody; scFv.
XX
XX Synthetic.
OS
XX

```

```

PN WO9920749-A1.
XX
XX 29-APR-1999.
PD
XX
XX 20-OCT-1998; 98WO-GB03135.
PE
XX 21-NOV-1997; 97US-0066729.
PR 20-OCT-1997; 97GB-0022131.
PR 13-NOV-1997; 97US-0065428.
XX
XX (MEDT-) MEDICAL RES COUNCIL.
PA
XX Tomlinson I, Winter G;
PI
XX WPI, 1999-288302/24.
DR
XX
XX Screening for functional polypeptides which bind a ligand
PT
XX
XX Example 3; Fig 4; 67pp; English.
PS
XX
XX The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in
CC diagnostic, prophylactic and therapeutic procedures. AAY02473-Y02525
CC represent clones selected after panning primary and somatic NNK
CC libraries with 5 antigens (bovine ubiquitin, rat BIP, bovine histone,
CC NIP-BSA and hen egg lysozyme).
CC
XX
XX Sequence 56 AA;
SQ

```

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Query Match 100.0%; Score 86; DB 20; Length 56;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AISGSGSTYYADSVKG 17
   |||||||
Db 6 aisgsgstyadsvkg 22

```

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RESULT 15
AAY02505
ID AAY02505 standard; Protein; 56 AA.
XX
XX AAY02505;
AC
XX
XX 15-JUL-1999 (first entry)
DT
XX
XX Clone selected after panning a NNK library of the invention.
DE
XX Screening; functional polypeptide; ligand; non-functional;
RW enrichment; single chain antibody; scFv.
XX
XX Synthetic.
OS
XX
XX WO9920749-A1.
PN
XX
XX 29-APR-1999.
PD
XX
XX 20-OCT-1998; 98WO-GB03135.
PE
XX 21-NOV-1997; 97US-0066729.
PR 20-OCT-1997; 97GB-0022131.
PR 13-NOV-1997; 97US-0065428.
XX

```

PA (MEDI-) MEDICAL RES COUNCIL.

PI Tomlinson I, Winter G;

DR WPI: 1999-288302/24.

PT Screening for functional polypeptides which bind a ligand

PS Example 3; Fig 4; 67pp; English.

88

CC repertoire of polypeptides with a generic ligand, and then screening

CC permits the removal from a chosen repertoire of polypeptides, those

CC frame-shift mutations, stop codons, folding mutants or expression

CC ligand. The method also permits the enrichment of a chosen repertoire

CC and highly expressed. The polypeptides obtained can be used in

CC represent clones selected after panning primary and somatic NKK

CC NIP-BSA and hen egg lysozyme).
VV

sq sequence 56 AA;

Query Match 100 0%: Score 86: DB 20: Length 56:

```
Best Local Similarity 100.0%; Pred. NO: 7e-06;
Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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ov 1 AIGSGGTTYADSVKG 17 .

Db 6 a i s s a q s t v y a d s v k a 2 2

Search completed: June 21, 2002, 09:20:16

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:46 ; Search time 84.18 Seconds

(without alignments)
4.933 Million cell updates/sec

Title: US-09-780-035-28_COPY_40_56

Perfect score: 86

Sequence: 1 A1SGSGSTYADSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	116	4	US-08-983-607-36
2	86	100.0	117	3	US-08-545-809A-109
3	86	100.0	117	4	US-08-983-607-46
4	86	100.0	118	2	US-08-652-816A-12
5	86	100.0	120	4	US-09-025-769B-38
6	86	100.0	120	4	US-09-025-769B-63
7	86	100.0	123	2	US-08-428-197-38
8	86	100.0	123	5	PCT-US93-10555-38
9	86	100.0	124	4	US-08-983-607-51
10	86	100.0	125	1	US-08-478-039-99
11	86	100.0	125	1	US-08-476-342A-99
12	86	100.0	125	2	US-08-428-197-1
13	86	100.0	125	5	PCT-US93-10555-1
14	86	100.0	131	4	US-08-983-607-28
15	86	100.0	140	4	US-08-983-607-32
16	86	100.0	144	1	US-08-026-320A-2
17	86	100.0	281	4	US-09-025-769B-178
18	83	96.5	122	4	US-08-958-201-6
19	83	96.5	126	2	US-08-983-607-26
20	82	95.3	98	5	US-08-428-197-48
21	82	95.3	98	5	PCT-US93-10555-48
22	82	95.3	119	4	US-08-983-607-22
23	81	94.2	116	2	US-08-428-197-2
24	81	94.2	116	5	PCT-US93-10555-2
25	78	90.7	113	3	US-08-974-899-6
26	78	90.7	122	3	US-07-934-373C-21
27	78	90.7	122	3	US-08-437-642B-21

28	78	90.7	122	5	PCT-US93-07832-21	Sequence 21, Appl
29	77	89.5	17	1	US-08-264-093-22	Sequence 22, Appl
30	77	89.5	118	2	US-08-652-816A-11	Sequence 11, Appl
31	77	89.5	120	1	US-08-264-093-14	Sequence 14, Appl
32	76	88.4	117	2	US-08-428-197-36	Sequence 36, Appl
33	76	88.4	117	5	PCT-US93-10555-36	Sequence 36, Appl
34	76	88.4	120	2	US-08-428-197-20	Sequence 20, Appl
35	76	88.4	120	2	US-08-428-197-22	Sequence 22, Appl
36	76	88.4	120	2	US-08-428-197-24	Sequence 24, Appl
37	76	88.4	120	2	US-08-428-197-26	Sequence 26, Appl
38	76	88.4	120	2	US-08-428-197-28	Sequence 28, Appl
39	76	88.4	120	2	US-08-428-197-30	Sequence 30, Appl
40	76	88.4	120	2	US-08-428-197-32	Sequence 32, Appl
41	76	88.4	120	2	US-08-428-197-34	Sequence 34, Appl
42	76	88.4	120	2	US-08-428-197-40	Sequence 40, Appl
43	76	88.4	120	5	PCT-US93-10555-20	Sequence 20, Appl
44	76	88.4	120	5	PCT-US93-10555-22	Sequence 22, Appl
45	76	88.4	120	5	PCT-US93-10555-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-983-607-36
Sequence 36, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Kinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes

IMMEDIATE SOURCE:
LIBRARY: DM414 scfv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: V474
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-36

Query Match 100.0%; Score 86; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 A1SGSGSTYYADSVKG 17
|||||
DB 50 A1SGSGSTYYADSVKG 66

RESULT 2
US-08-545-809A-109

Sequence 109, Application US/08545809A
Patent No. 6096878

GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku

APPLICANT: Matsuda, Fumihiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,809A

FILING DATE: 27-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 06501/004001

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ. ID NO: 109:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-545-809A-109

Query Match 100.0%; Score 86; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 A1SGSGSTYYADSVKG 17
|||||
DB 69 A1SGSGSTYYADSVKG 85

RESULT 3

US-08-983-607-46

Sequence 46, Application US/08983607

Patent No. 6140470

GENERAL INFORMATION:

APPLICANT: Alan Garen

APPLICANT: Xiaohong Cai

TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-

TITLE OF INVENTION: bodies

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Department of Molecular Biophysics

ADDRESSEE: and Biochemistry, Yale University

STREET: 266 Whitney Avenue

CITY: New Haven

STATE: Connecticut

COUNTRY: United States of America

ZIP: 06520-8114

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" 1.44 Mb diskette

COMPUTER: IBM PC

OPERATING SYSTEM: MS DOS

SOFTWARE: Word Processing

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983,607

FILING DATE: April 27, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB96/01032

FILING DATE: June 28, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mary M. Krinsky

REGISTRATION NUMBER: 32423

REFERENCE/DOCKET NUMBER: OCR-679

TELEPHONE: 203-773-1183

TELEFAX: 203-773-9544

INFORMATION FOR SEQ. ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 residues

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

DESCRIPTION: polypeptide

ORIGINAL SOURCE:

ORGANISM: Homo sapiens (melanoma patient

INDIVIDUAL ISOLATE: immunized with autologous tumor cells)

INDIVIDUAL ISOLATE: peripheral blood lympho-

IMMEDIATE SOURCE: cytes

LIBRARY: VH antibodies obtained from fuses

LIBRARY: fusion phage construct

CLONE: C55

FEATURE:

NAME/KEY: heavy chain

US-08-983-607-46

Query Match 100.0%; Score 86; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 A1SGSGSTYYADSVKG 17
|||||
DB 50 A1SGSGSTYYADSVKG 66

RESULT 4

APPLICANT: Oshbourn, JK
APPLICANT: Allen, Du
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-12

Query Match 100.0%; Score 86; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A1SGSGSTYYADSVKG 17
|||||

Db 50 A1SGSGSTYYADSVKG 66

RESULT 5
US-09-025-769B-38
Sequence 38, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter
APPLICANT: Ilaq, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)565-9000
TELEFAX: (212)565-9090
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-38

Query Match 100.0%; Score 86; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A1SGSGSTYYADSVKG 17
|||||

Db 50 A1SGSGSTYYADSVKG 66

RESULT 6
US-09-025-769B-63
Sequence 63, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilaq, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9030
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-63

Query Match 100.0%; Score 86; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A1SGSGSTYYADSVKG 17
|||||
DB 50 A1SGSGSTYYADSVKG 66

RESULT 7
US-08-428-197-38
Sequence 38, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Judas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-197-38

Query Match 100.0%; Score 86; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A1SGSGSTYYADSVKG 17
|||||
DB 50 A1SGSGSTYYADSVKG 66

RESULT 8
PCT-US93-10555-38
Sequence 38, Application PCT/US9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Judas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-10555-38

Query Match 100.0%; Score 86; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A1SGSGSTYYADSVKG 17
|||||
DB 50 A1SGSGSTYYADSVKG 66

RESULT 9
US-08-983-607-51
Sequence 51, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen

APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSER: Department of Molecular Biophysics
and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient
immunized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: cytes
IMMEDIATE SOURCE:
LIBRARY: VH antibodies obtained from fuses
CLONE: E-13
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-51

Query Match 100.0%; Score 86; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 A1SGSGSTYYADSVKG 17
|||||
DB 50 A1SGSGSTYYADSVKG 66

RESULT 10
US-08-478-039-99
Sequence 99, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 18/2
US-08-478-039-99

Query Match 100.0%; Score 86; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 A1SGSGSTYYADSVKG 17
|||||
DB 50 A1SGSGSTYYADSVKG 66

RESULT 11
US-08-476-349A-99
Sequence 99, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/476,349A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 514
: PRIORITY INFORMATION DATA:
: PRIORITY APPLICATION NUMBER: US 08/379,072
: FILING DATE: 25-JAN-1995
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/912,292
: FILING DATE: 10-JUL-1992
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/856,281
: FILING DATE: 23-MAR-1992
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/735,064
: FILING DATE: 25-JUL-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Teskin Esq., Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-161
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 99:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 125 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: POSITION IN GENOME:
: CHROMOSOME/SEGMENT: 18/2
: US-08-476-349A-99

Query Match      100.0%; Score 86; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 A1SGSGSTYYADSVKG 17
        |||
Db      50 A1SGSGSTYYADSVKG 66

RESULT 12
US-08-428-197-1
: Sequence 1, Application US/08428197
: Patent No. 5891438
: GENERAL INFORMATION:
: APPLICANT: SILVERMAN, GREGG J.
: TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
: TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
: TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Spensley Horn Judas & Lubitz
: STREET: 1880 Century Park East - Suite 500
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
```

```

: APPLICATION NUMBER: US/08/428,197
: FILING DATE:
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/10555
: FILING DATE: 29-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Howells, Stacy L.
: REGISTRATION NUMBER: 34,842
: REFERENCE/DOCKET NUMBER: PD-2630
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 455-5100
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 125 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: IMMEDIATE SOURCE:
: CLONE: 18/2
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..125
: US-08-428-197-1

Query Match      100.0%; Score 86; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 A1SGSGSTYYADSVKG 17
        |||
Db      50 A1SGSGSTYYADSVKG 66

RESULT 13
PCT-US93-10555-1
: Sequence 1, Application PC/TUS9310555
: GENERAL INFORMATION:
: APPLICANT: SILVERMAN, GREGG J.
: TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
: TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
: TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Spensley Horn Judas & Lubitz
: STREET: 1880 Century Park East - Suite 500
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/10555
: FILING DATE: 29-OCT-1993
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Howells, Stacy L.
: REGISTRATION NUMBER: 34,842
: REFERENCE/DOCKET NUMBER: PD-2630
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 455-5100
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 125 amino acids
```



```

: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: IMMEDIATE SOURCE:
: CLONE: 18/2
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1..125
: PCT-US93-10555-1

Query Match          100.0%; Score 86; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A1SGSGSTYYADSVKG 17
Db 50 A1SGSGSTYYADSVKG 66

RESULT 14
US-08-983-607-28
: Sequence 28, Application US/08983607
: Patent No. 6140470
: GENERAL INFORMATION:
: APPLICANT: Alan Garen
: APPLICANT: Xiaohong Cai
: TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
: TITLE OF INVENTION: bodies
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Department of Molecular Biophysics
: ADDRESSEE: and Biochemistry, Yale University
: STREET: 266 Whitney Avenue
: CITY: New Haven
: STATE: Connecticut
: COUNTRY: United States of America
: ZIP: 06520-8114
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" 1.44 Mb diskette
: COMPUTER: IBM PC
: OPERATING SYSTEM: MS DOS
: SOFTWARE: Word Processing
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/983,607
: FILING DATE: April 27, 1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/IB96/01032
: FILING DATE: June 28, 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Mary M. Krinsky
: REGISTRATION NUMBER: 32423
: REFERENCE/DOCKET NUMBER: OCR-679
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 203-773-9544
: TELEFAX: 203-773-1183
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 131 residues
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE:
: DESCRIPTION: polypeptide
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens (melanoma patient immu-
: ORGANISM: nized with autologous tumor cells)
: INDIVIDUAL ISOLATE: peripheral blood lymphocytes
: IMMEDIATE SOURCE:
: LIBRARY: DM414 scFv antibodies obtained from
```

```

: LIBRARY: fuses fusion phage construct
: CLONE: V13
: FEATURE:
: NAME/KEY: heavy chain
: US-08-983-607-28

Query Match          100.0%; Score 86; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A1SGSGSTYYADSVKG 17
Db 50 A1SGSGSTYYADSVKG 66

RESULT 15
US-08-983-607-32
: Sequence 32, Application US/08983607
: Patent No. 6140470
: GENERAL INFORMATION:
: APPLICANT: Alan Garen
: APPLICANT: Xiaohong Cai
: TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
: TITLE OF INVENTION: bodies
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Department of Molecular Biophysics
: ADDRESSEE: and Biochemistry, Yale University
: STREET: 266 Whitney Avenue
: CITY: New Haven
: STATE: Connecticut
: COUNTRY: United States of America
: ZIP: 06520-8114
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" 1.44 Mb diskette
: COMPUTER: IBM PC
: OPERATING SYSTEM: MS DOS
: SOFTWARE: Word Processing
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/983,607
: FILING DATE: April 27, 1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/IB96/01032
: FILING DATE: June 28, 1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Mary M. Krinsky
: REGISTRATION NUMBER: 32423
: REFERENCE/DOCKET NUMBER: OCR-679
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 203-773-9544
: TELEFAX: 203-773-1183
: INFORMATION FOR SEQ ID NO: 32:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 140 residues
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE:
: DESCRIPTION: polypeptide
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens (melanoma patient immu-
: ORGANISM: nized with autologous tumor cells)
: INDIVIDUAL ISOLATE: peripheral blood lymphocytes
: IMMEDIATE SOURCE:
: LIBRARY: DM414 scFv antibodies obtained from
: LIBRARY: fuses fusion phage construct
: CLONE: V86
: FEATURE:
: NAME/KEY: heavy chain and linker
: US-08-983-607-32
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Query Match 100.0%; Score 86; DB 4; Length 140;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AISGGGSGTYADSVKG 17
 |||||
 Db 50 AISGGGSGTYADSVKG 66

Search completed: June 21, 2002, 09:21:46
 Job time: 409 sec

GenCore version 4.5
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OM protein - protein search, using sw model

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Run on:      June 21, 2002, 09:20:16 ; Search time 245.49 Seconds
              (without alignments)
              4.072 Million cell updates/sec
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Title: US-09-780-035-28_COPY_89_97
Perfect score: 56
Sequence: 1 DDDDYDFDY 9
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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15:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT *	
16:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT *	
17:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT *	
18:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT *	
19:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT *	
20:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT *	
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22:	/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT *	

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	56	100.0	9	22	AAG65312	Anti-IL-18 antiBooB
2	56	100.0	108	22	AAG65318	Anti-IL-18 antiBooB
3	56	100.0	118	22	AAG65354	Anti-IL-18 antiBooB
4	56	100.0	235	22	AAG65320	Anti-IL-18 antiBooB
5	46	82.1	1186	22	AAB50654	C. elegans APR-1 p
6	44	78.6	273	20	AAV36976	Amino acid sequenc
7	44	78.6	515	18	AAW31547	Bloom's syndrome B
8	44	78.6	739	18	AAW31549	Bloom's syndrome B
9	44	78.6	1417	18	AAW31548	Bloom's syndrome B
10	44	78.6	1417	18	AAW31550	Bloom's syndrome B
11	44	78.6	1417	18	AAW31551	Bloom's syndrome B

12	44	78.6	1.18	18	AAW15264	Bloom syndrome act
13	43	76.8	295	21	AAG11294	Arbidopsis thaliaa
14	43	76.8	297	21	AAAG49229	Arbidopsis thaliaa
15	43	76.8	378	21	AAAG11293	Arbidopsis thaliaa
16	43	76.8	380	21	AAAG49228	Arbidopsis thaliaa
17	43	76.8	416	21	AAAG11292	Arbidopsis thaliaa
18	43	76.8	416	21	AAAG49227	Arbidopsis thaliaa
19	43	76.8	492	20	AAAG56281	Babesia microti BM
20	43	76.8	492	20	AAW24342	Babesia microti BM
21	43	76.8	492	21	AAAB30191	B. microti BMN-4
22	43	76.8	503	19	AAAB56302	Babesia microti NM
23	43	76.8	503	20	AAAY24364	Babesia microti an
24	43	76.8	503	20	AAAB30216	B. microti clone a
25	41.5	74.1	57	21	AAAG11037	Arbidopsis thaliaa
26	41.5	74.1	183	21	AAAG54281	Arbidopsis thaliaa
27	41.5	74.1	184	21	AAAG54280	Arbidopsis thaliaa
28	41.5	74.1	206	21	AAAG54279	Arbidopsis thaliaa
29	41.5	74.1	541	21	AAAG53734	Arbidopsis thaliaa
30	41.5	74.1	554	21	AAAG53733	Arbidopsis thaliaa
31	41.5	74.1	668	21	AAAG53732	Arbidopsis thaliaa
32	32	73.2	97	22	AAAM00012	ER. binding domain
33	41	73.2	136	22	ABBI11180	Human pancreatic ph
34	41	73.2	318	22	ABG223348	Arbidopsis thaliaa
35	41	73.2	330	22	AAAG223347	Arbidopsis thaliaa
36	41	73.2	806	22	AAAB94052	Human protein sequ
37	41	73.2	846	22	AAU38311	Salmonella typhi c
38	41	73.2	1809	22	AAAE3101	Human phospholipase
39	40	71.4	183	22	ABAB68544	Drosophila melanoid
40	40	71.4	217	21	AAAG52441	Arbidopsis thaliaa
41	40	71.4	246	22	AAUA3222	Propionibacterium
42	40	71.4	429	22	ABAB5976	Phosphatidyl melano
43	40	71.4	700	16	AAAT70235	P. falciparum EBL-
44	40	71.4	700	16	AAAT70235	P. falciparum ebl-2.
45	40	71.4	700	21	AAAT77903	P. falciparum ebl-1

ALIGNMENTS

XX	RESULT	1	
XX	AAG65312		
ID	AAG65312	standard; protein; 9 AA.	
XX			
AC	AAG65312;		
XX			
DT	30-NOV-2001	(first entry)	
XX			
DE	Anti-IL-18 antibody LT28 heavy chain CDRI fragment.		
XX			
IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;			
KW	neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiact;		
KW	immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200158956-A2.		
XX			
PD	16-AUG-2001.		
XX			
PF	09-FEB-2001; 2001WO-US04170.		
XX			
PR	10-FEB-2000; 2000US-0181608.		
XX			
PA	(BADI) BASF AG.		
XX			
PI	Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfield J;		
PI	Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;		
PI	Lenard SN;		
XX			
DR	WPI; 2001-550020/61.		
XX			
PT	Novel interleukin-18 and compounds capable of binding to human		
PT	interleukin-18 useful for treating, e.g., inflammatory disorders,		

PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Claim 32; Page 41; 91pp; English.
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LT28
 CC heavy chain CDR3 fragment.
 CC
 SQ Sequence 9 AA:
 Query Match 100.0%; Score 56; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DDDDYDFDY 9
 Db 1 ddddydfdy 9
 RESULT 2
 AAG65318 100.0%; Score 56; DB 22; Length 9;
 ID AAG65318 standard; protein; 108 AA.
 AC AAG65318;
 XX
 DT 30-NOV-2001 (first entry)
 DE Anti-IL-18 antibody LT28 heavy chain sequence.
 XX
 KM IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KM nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KM immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 DR WPI; 2001-550020/61.
 DR N-PSDB; AAH47513.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Example 2; Page 41; 91pp; English.

XX
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LT28
 CC heavy chain sequence.
 CC
 SQ Sequence 108 AA:
 Query Match 100.0%; Score 56; DB 22; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DDDDYDFDY 9
 Db 89 ddddydfdy 97
 RESULT 3
 AAG65354 100.0%; Score 56; DB 22; Length 108;
 ID AAG65354 standard; protein; 118 AA.
 AC AAG65354;
 XX
 DT 30-NOV-2001 (first entry)
 DE Anti-IL-18 antibody LT28 heavy chain sequence.
 XX
 KM IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KM nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KM immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 DR WPI; 2001-550020/61.
 DR N-PSDB; AAH47513.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Claim 1; Page 89; 91pp; English.
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a

disorder where IL-18 is detrimental in, a human subject suffering from, CC
 inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease, CC
 inflammatory bowel disease, and osteoarthritis), neurological disorders CC
 (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and CC
 stroke), heart failure, myocardial infarction, autoimmune diseases such CC
 as autoimmune hepatitis and autoimmune neutropenia, and mental disorders CC
 (e.g., depression and schizophrenia). Treatment with an anti-IL-18 CC
 antibody may occur before, concurrent, or after administration of a CC
 second agent selected from an antibody, or fragment, capable of binding CC
 human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids, CC
 cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory CC
 agents. The present sequence represents an anti-IL-18 antibody LT28 CC
 heavy chain sequence. CC
 XX

SO Sequence 118 AA;

Query Match 100.0%; Score 56; DB 22; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDDYDFDY 9
 |||||
 Db 99 ddddydfdy 107

RESULT 4

AAG65320 ID AAG65320 standard; protein; 235 AA.

AC AAG65320;

DT 30-NOV-2001 (first entry)

DE Anti-IL-18 antibody LT28 sequence.

IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiac;
 KM immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.

OS Homo sapiens.

PN WO200158956-A2.

PD 16-AUG-2001.

PF 09-FEB-2001; 2001WO-US04170.

PR 10-FEB-2000; 2000US-0181608.

PA (BAD1) BASF AG.

PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;

DR WPI; 2001-550020/61.

Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -

PS Examples; Page 79-80; 91pp; English.

The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such

as autoimmune hepatitis and autoimmune neutropenia, and mental disorders CC
 (e.g., depression and schizophrenia). Treatment with an anti-IL-18 CC
 antibody may occur before, concurrent, or after administration of a CC
 second agent selected from an antibody, or fragment, capable of binding CC
 human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids, CC
 cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory CC
 agents. The present sequence represents an anti-IL-18 antibody LT28 CC
 comprising the heavy chain and light chain sequences joined by a linker. CC
 XX

SO Sequence 235 AA;

Query Match 100.0%; Score 56; DB 22; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDDYDFDY 9
 |||||
 Db 89 ddddydfdy 97

RESULT 5

AAB50654 ID AAB50654 standard; protein; 1186 AA.

AC AAB50654;

DT 19-MAR-2001 (first entry)

DE C. elegans APR-1 protein sequence SEQ ID NO:16.

Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
 KW protein-protein interaction; identification.

OS Caenorhabditis elegans.

PN WO200073328-A2.

PD 07-DEC-2000.

PF 02-JUN-2000; 2000WO-EP05108.

PR 01-JUN-1999; 99GB-0012755.

PA (DEYG-) DEYGEN NV.

PI Van Criekinge W, Roelens I, Bogaert T, Verwaerde P;

DR WPI; 2001-016508/02.

DR N-PSDB; AAC90920.

Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and
 PT a human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
 PT identifying unknown human cDNAs which encode proteins that interact
 PT with the human unc-5C protein -

PS Claim 39; Page 122-126; 246pp; English.

The present invention describes 3 variants of human unc-5C cDNAs
 CC (unc-5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced
 CC unc-5C transcripts, and a human unc-5HS1 cDNA which shares homology with
 CC the Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on
 CC protein-protein interactions between the unc-5 protein and a variety of
 CC different interacting proteins. The unc-5C variant cDNAs and a variety of
 CC cDNA are useful in methods for identifying compounds which reduce or
 CC inhibit the lethal phenotype associated with the expression of the
 CC unc-5 death domain in yeast. They are also useful in yeast two hybrid
 CC experiments for identifying unknown human cDNAs which encode proteins
 CC that interact with the human unc-5C protein. AAC90914 to AAC90971 and
 CC AAB50646 to AAB50693 represent sequences used in the exemplification of
 CC the present invention.

SO Sequence 1186 AA;

Query Match 82.1%; Score 46; DB 22; Length 1186;
 Best Local Similarity 77.8%; Pred. No. 67;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DDDDYDFDY 9
 |||||:|
 Db 964 ddddydyty 972

RESULT 6

AAV36976
 ID AAV36976 standard; Protein; 273 AA.

AC AAV36976;

DT 07-OCT-1999 (first entry)

DE Amino acid sequence of a Chlamydia trachomatis protein.

XX Vaccines: eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perithenarthritis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
 KW Bartholinitis; pneumonia; venereal lymphogranulomatosis.

OS Chlamydia trachomatis.

PN W0928475-A2.

PD 10-JUN-1999.

PF 27-NOV-1998; 98WC-IB01939.

PR 04-NOV-1998; 98US-0107077.

PR 28-NOV-1997; 97FR-0015041.

PR 17-DEC-1997; 97FR-0016034.

PA (GEST) GENSET.

PI Griffiths R;

DR WPI; 1999-371125/31.

PT Genome sequence of Chlamydia trachomatis

PS Disclosure; Page 815-816; 1755pp; English.

XX AAV36754-Y37949 are encoded by open reading frames (ORFs) of the genome
 CC of Chlamydia trachomatis (see AA201425). The polypeptides can be used as
 CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
 CC can also be used to control growth of the microorganism. Chlamydia
 CC trachomatis is responsible for a large number of diseases, e.g. eye
 CC diseases such as conventional trachoma, nonendemic trachoma,
 CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
 CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
 CC perithenarthritis, Bartholinitis; pneumonia in breast feeding infants;
 CC and venereal lymphogranulomatosis. The polypeptides of the invention
 CC may be of use in treating these diseases.

XX Sequence 273 AA;

Query Match 78.6%; Score 44; DB 20; Length 273;

Best Local Similarity 77.8%; Pred. No. 30;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DDDDYDFDY 9
 |||||:|
 Db 261 ddddydfny 269

RESULT 7

AAW31547
 ID AAW31547 standard; Protein; 515 AA.

AC AAW31547;

DT 27-JAN-1998 (first entry)

DE Bloom's syndrome BLM mutated protein.

DE BLM, Bloom's syndrome; BS; mutant; truncation; therapy; diagnosis.

OS Homo sapiens.

Key Location/Qualifiers

FT Protein

FT 1..515
 FT /note= "The insertion of a bp A at position 1610 of
 the wild type HI-5' BLM gene results in the
 insertion of a novel codon for Lys after amino
 acid position 514 followed by a stop codon"

PN W09717979-A1.

PD 22-MAY-1997.

PF 15-NOV-1996; 96WO-US19046.

PR 15-NOV-1995; 95US-0559303.

PA (NBL-) NEW YORK BLOOD CENT INC.

PI Ellis N, German J, Groden J;

DR WPI; 1997-289051/26.

DR N-PSDB; AAT93391.

PT Diagnosing Bloom's syndrome, and carriers, by detecting mutant BLM

PT genes - for gene therapy with nucleic acid encoding active BLM

PT protein to treat Bloom's syndrome and cancer in general

PS Disclosure; Page -; 51pp; English.

XX This is a truncated BLM protein encoded by a mutant gene sequence
 CC isolated from a Japanese Bloom's Syndrome sufferer designated
 CC "93(Yoya)". The insertion of a bp A at the position 1610 in the wild
 CC type HI-5' BLM gene results in the insertion of a novel codon for Lysine
 CC after amino acid position 514 followed by a stop codon.
 CC This was one of the seven unique mutations which were identified in
 CC a study of 10 people with Bloom's Syndrome. Based on the various
 CC mutations, diagnostic tests for Bloom's Syndrome have been developed
 CC which use standard sequence analysis techniques to detect the presence
 CC of 2 mutated BLM genes or the absence of a wild-type BLM gene.
 CC Note: The present sequence does not appear in the specification; it
 CC has been made by modifying the HI-5' wild type BLM sequence which is
 CC provided in Figure 2 (AAW15264).

XX Sequence 515 AA;

Query Match 78.6%; Score 44; DB 18; Length 515;

Best Local Similarity 77.8%; Pred. No. 57;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DDDDYDFDY 9
 |||||:|
 Db 292 ddddydtatf 300

RESULT 8

AAW31549
 ID AAW31549 standard; Protein; 739 AA.

AC AAW31549;

XX

DT	27-JAN-1998	(first entry)
XX		
DE	Bloom's syndrome BLM mutated protein.	
KM	BLM; Bloom's syndrome; BS; mutant; truncation; therapy; diagnosis.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	Protein	1..739
FT	/note=	"Deletion of ATCTGA from the wild type HI-5' BLM gene and insertion of TAGATTC results in the insertion of the novel codons for LDR after amino acid position 735 followed by a stop codon"
XX		
PN	W09717979-A1.	
PD	22-MAY-1997.	
XX		
PF	15-NOV-1996;	96WO-US19046.
XX		
PR	15-NOV-1995;	95US-0559303.
XX		
PA	(NYBL-) NEW YORK BLOOD CENT INC.	
XX		
PI	Ellis N, German J, Groden J;	
XX		
DR	WPI; 1997-289051/26.	
DR	N-PSDB; AAT93393.	
XX		
PT	Diagnosing Bloom's syndrome, and carriers, by detecting mutant BLM genes - for gene therapy with nucleic acid encoding active BLM protein to treat Bloom's syndrome and cancer in general	
XX		
PS	Disclosure; Page -: 51pp; English.	
XX		
CC	This is a truncated BLM protein encoded by a mutant gene sequence isolated from a Ashkenazi Jewish Bloom's Syndrome sufferer designated "15(Mark)". The deletion of ATCTGA from the wild type HI-5' BLM gene and insertion of TAGATTC results in the insertion of the novel codons for LDR after amino acid position 735 followed by a stop codon.	
CC	This was one of the seven unique mutations which were identified in a study of 10 people with Bloom's Syndrome. Based on the various mutations, diagnostic tests for Bloom's Syndrome have been developed which use standard sequence analysis techniques to detect the presence of 2 mutated BLM genes or the absence of a wild-type BLM gene.	
CC	Note: The present sequence does not appear in the specification; it has been made by modifying the HI-5' wild type BLM sequence which is provided in Figure 2 (AAHI5264).	
CC		
XX		
S0	Sequence	739 AA;
	Query Match	78.6%; Score 44; DB 18; Length 739;
	Best Local Similarity	77.8%; Pred. No. 82;
	Matches	7; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
OY	1 DDDDXDFDY 9	
	1;	
	292 ddddydtcf 300	
DB		
RESULT	9	
AAHI548		
ID	AAHI548 standard; Protein; 1417 AA.	
XX		
AC	AAHI548;	
XX		
DT	27-JAN-1998 (first entry)	
XX		
DE	Bloom's syndrome BLM mutated protein.	
XX		
KM	BLM; Bloom's syndrome; BS; mutant; therapy; diagnosis.	

[illegible]

```

FT Misc-difference 841
FT /label= 1841t
FT /note= "wild type Isoleucine is replaced by Threonine"
XX
XX
XX WO9717979-A1.
XX
XX PD 22-MAY-1997.
XX
XX PF 15-NOV-1996; 96MO-US19046.
XX
XX PR 15-NOV-1995; 95US-0559303.
XX
XX (NYBL-) NEW YORK BLOOD CENT INC.
XX
XX PI Ellis N, German J, Groden J;
XX
XX WPI; 1997-289051/26.
XX
XX N-PSDB; AAT93394.
XX
XX PT Diagnosing Bloom's syndrome, and carriers, by detecting mutant BLM
XX PT genes - for gene therapy with nucleic acid encoding active BLM
XX PT protein to treat Bloom's syndrome and cancer in general
XX
XX PS Disclosure; Page -, 51pp; English.
XX
XX CC This is a mutated BLM protein encoded by a mutant gene sequence isolated
XX CC from an Italian Bloom's Syndrome sufferer designated "92(VaB1)". The
XX CC substitution of the bp T at the position 2596 of the wild type H1-5'
XX CC gene to the bp C results in the amino acid Threonine at the position
XX CC 841. This is one of the seven unique mutations which were identified in
XX CC a study of 10 people with Bloom's Syndrome. Based on the various
XX CC mutations, diagnostic tests for Bloom's Syndrome have been developed
XX CC which use standard sequence analysis techniques to detect the presence
XX CC of 2 mutated BLM genes or the absence of a wild-type BLM gene.
XX CC Note: The present sequence does not appear in the specification; it
XX CC has been made by modifying the H1-5' wild type BLM sequence which is
XX CC provided in Figure 2 (AAT67013).
XX
XX SQ Sequence 1417 AA;

Query Match 78.6%; Score 44; DB 18; Length 1417;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDDDYDFDY 9
Db 292 ddddydtdf 300

RESULT 11
AAW31551
ID AAW31551 standard; Protein; 1417 AA.
XX
XX AC AAW31551;
XX
XX DT 27-JAN-1998 (first entry)
XX
XX DE Bloom's syndrome BLM mutated protein.
XX
XX KW BLM; Bloom's syndrome; BS; mutant; mutation; deletion;
XX KW therapy; diagnosis; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1055 /label= C10555
XX FT /note= "wild type Cys is replaced by Ser"
XX
XX PN WO9717979-A1.
XX
XX PD 22-MAY-1997.

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XX
XX PF 15-NOV-1996; 96MO-US19046.
XX
XX PR 15-NOV-1995; 95US-0559303.
XX
XX (NYBL-) NEW YORK BLOOD CENT INC.
XX
XX PI Ellis N, German J, Groden J;
XX
XX WPI; 1997-289051/26.
XX
XX N-PSDB; AAT93395.
XX
XX PT Diagnosing Bloom's syndrome, and carriers, by detecting mutant BLM
XX PT genes - for gene therapy with nucleic acid encoding active BLM
XX PT protein to treat Bloom's syndrome and cancer in general
XX
XX PS Disclosure; Page -, 51pp; English.
XX
XX CC This is a mutated BLM protein encoded by a mutant gene sequence isolated
XX CC from an Italian Bloom's Syndrome sufferer designated "113(Dadem)". The
XX CC substitution of the bp G at the position 3238 of the wild type H1-5'
XX CC gene to the bp C results in the amino acid Serine at the position 1055.
XX CC This is one of the seven unique mutations which were identified in
XX CC a study of 10 people with Bloom's Syndrome. Based on the various
XX CC mutations, diagnostic tests for Bloom's Syndrome have been developed
XX CC which use standard sequence analysis techniques to detect the presence
XX CC of 2 mutated BLM genes or the absence of a wild-type BLM gene.
XX CC Note: The present sequence does not appear in the specification; it
XX CC has been made by modifying the H1-5' wild type BLM sequence which is
XX CC provided in Figure 2 (AAT67013).
XX
XX SQ Sequence 1417 AA;

Query Match 78.6%; Score 44; DB 18; Length 1417;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDDDYDFDY 9
Db 292 ddddydtdf 300

RESULT 12
AAW15264
ID AAW15264 standard; Protein; 1418 AA.
XX
XX AC AAW15264;
XX
XX DT 26-JAN-1998 (first entry)
XX
XX DE Bloom syndrome active BLM protein.
XX
XX KW BLM; Bloom syndrome; BS; mutant; probe; PCR primer; cancer;
XX KW therapy; diagnosis; vector.
XX
XX OS Homo sapiens.
XX
XX PN WO9717979-A1.
XX
XX PD 22-MAY-1997.
XX
XX PF 15-NOV-1996; 96MO-US19046.
XX
XX PR 15-NOV-1995; 95US-0559303.
XX
XX (NYBL-) NEW YORK BLOOD CENT INC.
XX
XX PI Ellis N, German J, Groden J;
XX
XX WPI; 1997-289051/26.
XX
XX N-PSDB; AAT67013.
XX

```


PT Diagnosing Bloom's syndrome, and carriers, by detecting mutant BLM
PT genes - For gene therapy with nucleic acid encoding active BLM
PT protein to treat Bloom's syndrome and cancer in general
XX
PS Claim 58; Fig 2; 51pp; English.
XX
CC This active BLM protein is encoded by a 4437 bp BLM gene sequence.
CC This is used in diagnosing Bloom's syndrome where 2 mutated BLM genes
CC or the absence of a wild-type BLM gene in the nucleic acid of a subject
CC is detected. The BLM gene is in the 250 kb region between two markers
CC binding a 1.3 cm region on chromosome 15. cDNA from this region was
CC isolated, a 847 bp fragment selected and used to screen a HeLa cDNA
CC library. The longest clone H1 was isolated and extended by PCR to isolate
CC this BLM gene sequence. Delivery of a functional BLM gene to bone marrow
CC cells, e.g. via the viral vectors, is used to treat or prevent the onset
CC of Bloom's syndrome. Identification of the BLM gene and its products
CC should assist in the development of therapeutic and diagnostic agents for
CC cancer.
SQ Sequence 1418 AA;
XX
XX
Query Match 78.6%; Score 44; DB 18; Length 1418;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 DDDDDYDFDY 9
| | | | | | | | | |
Db 292 ddddytdtcf 300
RESULT 13
AG11294
ID AG11294 standard; Protein; 295 AA.
XX
AC AG11294;
XX
DF 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9958.
XX
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
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Query Match 76.8%; Score 43; DB 21; Length 295;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 48 dddedfd 56

RESULT 14
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ID AAG49229 standard; Protein: 297 AA.
XX
AC AAG49229;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 62256.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
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PD 06-SEP-2000.
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PR 26-OCT-1999; 9905-0161359.
PR 26-OCT-1999; 9905-0161360.
PR 26-OCT-1999; 9905-0161361.
PR 28-OCT-1999; 9905-0161920.
PR 28-OCT-1999; 9905-0161992.
PR 28-OCT-1999; 9905-0161993.
PR 29-OCT-1999; 9905-0162142.

Query Match 76.8%; Score 43; DB 21; Length 297;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDDDYDFDY 9
Dd 50 dddedfd 58

RESULT 15
AAG11293
ID AAG11293 standard; Protein: 378 AA.
XX
AC AAG11293;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9957.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
PR 23-MAR-1999; 9905-0125788.
PR 25-MAR-1999; 9905-0126264.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 28-APR-1999; 9905-0130891.
PR 30-APR-1999; 9905-0131449.
PR 30-APR-1999; 9905-0132048.
PR 04-MAY-1999; 9905-0132484.
PR 05-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 06-MAY-1999; 9905-0132487.
PR 07-MAY-1999; 9905-0132863.
PR 11-MAY-1999; 9905-0134296.
PR 14-MAY-1999; 9905-0134218.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134221.
PR 18-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134768.
PR 19-MAY-1999; 9905-0134941.
PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.

PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
PR 03-JUN-1999; 9905-0137528.
PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.
PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138540.
PR 10-JUN-1999; 9905-0138847.
PR 14-JUN-1999; 9905-0139152.
PR 16-JUN-1999; 9905-0139459.
PR 16-JUN-1999; 9905-0139453.
PR 17-JUN-1999; 9905-0139492.
PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139899.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 02-JUL-1999; 9905-0142154.
PR 06-JUL-1999; 9905-0142055.
PR 08-JUL-1999; 9905-0142390.
PR 09-JUL-1999; 9905-0142803.
PR 12-JUL-1999; 9905-0142920.
PR 13-JUL-1999; 9905-0143542.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.
PR 16-JUL-1999; 9905-0144086.
PR 19-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 21-JUL-1999; 9905-0144884.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.
PR 22-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
PR 23-JUL-1999; 9905-0145218.
PR 23-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.
PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
PR 02-AUG-1999; 9905-0146388.
PR 03-AUG-1999; 9905-0146389.
PR 04-AUG-1999; 9905-0147038.
PR 04-AUG-1999; 9905-0147204.

PR 04-AUG-1999: 99US-0147302.
 PR 05-AUG-1999: 99US-0147192.
 PR 05-AUG-1999: 99US-0147260.
 PR 06-AUG-1999: 99US-0147303.
 PR 06-AUG-1999: 99US-0147416.
 PR 09-AUG-1999: 99US-0147493.
 PR 09-AUG-1999: 99US-0147935.
 PR 10-AUG-1999: 99US-0148171.
 PR 11-AUG-1999: 99US-0148319.
 PR 12-AUG-1999: 99US-0148341.
 PR 13-AUG-1999: 99US-0148565.
 PR 16-AUG-1999: 99US-0148684.
 PR 17-AUG-1999: 99US-0149368.
 PR 18-AUG-1999: 99US-0149375.
 PR 20-AUG-1999: 99US-0149426.
 PR 20-AUG-1999: 99US-0149722.
 PR 20-AUG-1999: 99US-0149723.
 PR 23-AUG-1999: 99US-0149929.
 PR 23-AUG-1999: 99US-0149902.
 PR 23-AUG-1999: 99US-0149930.
 PR 25-AUG-1999: 99US-0150566.
 PR 26-AUG-1999: 99US-0150884.
 PR 27-AUG-1999: 99US-0151065.
 PR 27-AUG-1999: 99US-0151066.
 PR 27-AUG-1999: 99US-0151080.
 PR 30-AUG-1999: 99US-0151303.
 PR 31-AUG-1999: 99US-0151338.
 PR 01-SEP-1999: 99US-0151930.
 PR 07-SEP-1999: 99US-0152363.
 PR 10-SEP-1999: 99US-0153070.
 PR 13-SEP-1999: 99US-0153758.
 PR 15-SEP-1999: 99US-0154018.
 PR 16-SEP-1999: 99US-0154039.
 PR 20-SEP-1999: 99US-0154779.
 PR 22-SEP-1999: 99US-0155139.
 PR 23-SEP-1999: 99US-0155486.
 PR 24-SEP-1999: 99US-0155659.
 PR 28-SEP-1999: 99US-0156458.
 PR 29-SEP-1999: 99US-0156596.
 PR 04-OCT-1999: 99US-0157117.
 PR 05-OCT-1999: 99US-0157753.
 PR 06-OCT-1999: 99US-0157865.
 PR 07-OCT-1999: 99US-0158029.
 PR 08-OCT-1999: 99US-0158232.
 PR 12-OCT-1999: 99US-0158369.
 PR 13-OCT-1999: 99US-0159293.
 PR 13-OCT-1999: 99US-0159294.
 PR 13-OCT-1999: 99US-0159295.
 PR 14-OCT-1999: 99US-0159329.
 PR 14-OCT-1999: 99US-0159330.
 PR 14-OCT-1999: 99US-0159331.
 PR 14-OCT-1999: 99US-0159637.
 PR 14-OCT-1999: 99US-0159638.
 PR 18-OCT-1999: 99US-0159584.
 PR 21-OCT-1999: 99US-0160741.
 PR 21-OCT-1999: 99US-0160767.
 PR 21-OCT-1999: 99US-0160768.
 PR 21-OCT-1999: 99US-0160770.
 PR 21-OCT-1999: 99US-0160814.
 PR 21-OCT-1999: 99US-0160815.
 PR 22-OCT-1999: 99US-0160860.
 PR 22-OCT-1999: 99US-0160981.
 PR 22-OCT-1999: 99US-0160989.
 PR 25-OCT-1999: 99US-0161404.
 PR 25-OCT-1999: 99US-0161405.
 PR 25-OCT-1999: 99US-0161406.
 PR 26-OCT-1999: 99US-0161359.
 PR 26-OCT-1999: 99US-0161360.
 PR 26-OCT-1999: 99US-0161361.
 PR 28-OCT-1999: 99US-0161920.
 PR 28-OCT-1999: 99US-0161992.
 PR 28-OCT-1999: 99US-0161993.
 PR 29-OCT-1999: 99US-0162142.

Query Match 76.8%; Score 43; DB 21; Length 378;
 Best Local Similarity 77.8%; Pred. No. 59;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DDDYDFDY 9
 |||| |||:
 Db 131 ddddedfd 139

Search completed: June 21, 2002, 09:20:17
 Job time: 430 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:41 ; Search time 109.39 Seconds

(without alignments)
7.906 Million cell updates/sec

Title: US-09-780-035-28_COPY_89_97

Sequence: 1 DDDDDYDFDY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_71:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	85.7	1578	2	AD1512
2	48	85.7	1582	2	AC1153
3	46	82.1	1186	2	T23327
4	46	82.1	1188	2	T23330
5	45	80.4	957	2	S32903
6	44	78.6	1417	2	A57570
7	43	76.8	424	2	S11676
8	43	76.8	708	2	G96518
9	42.5	75.9	356	2	T41764
10	42	75.0	51	2	B81443
11	42	75.0	634	1	MZVZ48
12	42	75.0	634	1	E42503
13	42	75.0	771	2	T18131
14	42	75.0	1683	2	T30885
15	42	75.0	4550	2	T18440
16	41.5	74.1	206	2	T46194
17	41	73.2	142	2	D32880
18	41	73.2	257	2	S50288
19	41	73.2	274	2	T48819
20	41	73.2	336	2	T25440
21	41	73.2	527	2	T16022
22	41	73.2	804	2	T49575
23	41	73.2	840	2	AG0526
24	41	73.2	936	2	T23393
25	40	71.4	630	2	S37663
26	40	71.4	779	2	T25389
27	40	71.4	1082	2	S37837
28	40	71.4	1154	1	VG1H1B
29	40	71.4	1190	2	S47536

30	40	71.4	1293	2	S42402
31	40	71.4	1526	2	T13823
32	40	71.4	2182	2	T28634
33	40	71.4	2452	1	RNZQ2L
34	40	71.4	2457	2	T18492
35	39.5	70.5	844	1	ZPECPB
36	39.5	70.5	844	2	A96648
37	39.5	70.5	844	2	A85499
38	39	69.6	194	2	C69333
39	39	69.6	194	2	G83696
40	39	69.6	210	2	G97235
41	39	69.6	257	2	A34168
42	39	69.6	292	2	A28939
43	39	69.6	292	2	A36089
44	39	69.6	292	2	I52858
45	39	69.6	294	1	A32915

ALIGNMENTS

RESULT 1
AD1512
peptidoglycan bound protein (LPXTG motif) adhesin homolog lin0636 [imported] - Lister
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD1512
R:Glaser, P.; Franke, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1512
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1578 <GLA>
A:Cross-references: GB:AL592022; PIDN:CA95868.1; PID:916413076; GSPDB:GN00178
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: lin0636

Query Match 85.7%; Score 48; DB 2; Length 1578;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DDDDDYDFDY 9
Db 620 DDDDDYDFDY 628
RESULT 2
AC1153
adhesin homolog lmo0627 [imported] - Listeria monocytogenes (strain EBD-e)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC1153
R:Glaser, P.; Franke, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1153
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1582 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CA98705.1; PID:916410016; GSPDB:GN00177

A: Experimental source: strain EGD-e
C: Genetics:
A: Gene: lmo0627

Query Match 85.7%; Score 48; DB 2; Length 1582;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDDDYDFDY 9
|:|:|:|:|:|
DB 620 DEDDFDFDY 628

RESULT 3

T23327
adenomatous polyposis coli protein 1 - *Caenorhabditis elegans*

N: Alternate names: apr-1 protein

C: Species: *Caenorhabditis elegans*

C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C: Accession: T23327; 703822

R: Gardner, A.
submitted to the EMBL Data Library, July 1996

A: Reference number: Z19727

A: Accession: T23327

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA

A: Residues: 1-1186 <MIL>

A: Cross-references: EMBL:Z75712; PIDN: CAB00045.1; GSPDB: GN00019; CESP: K04G2.8a

A: Experimental source: clone K04G2

R: Rochelleau, C.E.; Downs, W.D.; Lin, R.; Wiltmann, C.; Bel, Y.; Cha, Y.H.; Ali, M.; Price, R.; Cell 90, 707-716, 1997

A: Title: Wnt signaling and an APC related gene specify endoderm in early *C. elegans* embryo

A: Reference number: Z15051; MUID: 97433081

A: Accession: T03822

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-1186 <ROC>

A: Cross-references: EMBL: AF013950; NID: g2338717; PIDN: AAC47747.1; PID: g2338718

A: Experimental source: strain Bristol

C: Genetics:

A: Gene: apr-1; CESP: K04G2.8a

A: Map position: 1

A: Introns: 61/3; 113/2; 355/3; 551/3; 1067/3; 1161/3

A: Note: apr-1

Query Match 82.1%; Score 46; DB 2; Length 1186;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDDDYDFDY 9
|:|:|:|:|:|

DB 964 DDDDYDFDY 972

RESULT 4

T23330
hypothetical protein K04G2.8b - *Caenorhabditis elegans*

C: Species: *Caenorhabditis elegans*

C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C: Accession: T23330

R: Gardner, A.
submitted to the EMBL Data Library, July 1996

A: Reference number: Z19727

A: Accession: T23330

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA

A: Residues: 1-1188 <MIL>

A: Cross-references: EMBL: Z75712; PIDN: CAB00048.1; GSPDB: GN00019; CESP: K04G2.8b

A: Experimental source: clone K04G2

C: Genetics:

A: Gene: CESP: K04G2.8b

A: Map position: 1
A: Introns: 61/3; 113/2; 355/3; 551/3; 1069/3; 1163/3

Query Match 82.1%; Score 46; DB 2; Length 1188;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDDDYDFDY 9
|:|:|:|:|:|
DB 966 DDDDYDFDY 974

RESULT 5

S32903
6-phosphofructokinase (EC 2.7.1.11) beta chain - yeast (*Kluyveromyces marxianus* var.

C: Species: *Kluyveromyces marxianus* var. *lactis*, *Candida sphaerica*

C: Date: 08-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999

C: Accession: S32903; S29603

R: Heinisch, J.; Kirchbach, L.; Liesen, T.; Vogelsang, K.; Hollenberg, C.P.

Mol. Microbiol. 8, 559-570, 1993

A: Title: Molecular genetics of phosphofructokinase in the yeast *Kluyveromyces lactis*.

A: Reference number: S32902; MUID: 93316853

A: Accession: S32903

A: Molecule type: DNA

A: Residues: 1-957 <HEI>

A: Cross-references: EMBL: Z17316; NID: g2881; PIDN: CAAT8964.1; PID: g2882

C: Genetics:

A: Gene: PFK2

C: Superfamily: human 6-phosphofructokinase; 6-phosphofructokinase 1 homology

C: Keywords: ATP; phosphotransferase

F: 178-489/Domain: 6-phosphofructokinase 1 homology <6PF1>

F: 567-860/Domain: 6-phosphofructokinase 1 homology <6PF2>

Query Match 80.4%; Score 45; DB 2; Length 957;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDDDYDFD 8
|:|:|:|:|:|
DB 871 DDDDYDFD 878

RESULT 6

A57570
Bloom's syndrome related protein BLM - human

C: Species: *Homo sapiens* (man)

C: Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 19-Jan-2001

C: Accession: A57570

R: Ellis, N.A.; Groden, J.; Ye, T.Z.; Straughen, J.; Lennon, D.J.; Cloccl, S.; Proytch

Cell 83, 655-666, 1995

A: Title: The Bloom's syndrome gene product is homologous to RecQ helicases.

A: Reference number: A57570; MUID: 96069866

A: Accession: A57570

A: Status: preliminary; not compared with conceptual translation

A: Molecule type: mRNA

A: Residues: 1-1417 <ELL>

A: Cross-references: GB: U39817; NID: g1072121; PIDN: AAA87850.1; PID: g1072122

C: Genetics:

A: Gene: GDB: BLM

A: Cross-references: GDB: 135698; OMIM: 210900

A: Map position: 15q26.1-15q26.1

C: Superfamily: Bloom's syndrome helicase; recQ helicase homology

C: Keywords: ATP; nucleotide binding; P-loop

F: 688-686/Region: nucleotide-binding motif A (P-loop)

F: 791-796/Region: nucleotide-binding motif B

F: 795-798/Region: DEAH motif

F: 1022-1066/Domain: recQ helicase homology <RHH>

Query Match 78.6%; Score 44; DB 2; Length 1417;
Best Local Similarity 77.8%; Pred. No. 61;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:48:16 ; Search time 52.75 Seconds

(without alignments)
6.606 Million cell updates/sec

Title: US-09-780-035-28_COPY_89_97

Perfect score: 56

Sequence: 1 DDDDYDFDY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	80.4	957	1 K6P2_KLUOLA	Q03216 Kluveromyc
2	44	78.6	1417	1 BLM_HUMAN	P54132 homo sapien
3	43	76.8	424	1 SP60_DICDI	P15270 dictyosteli
4	42	75.0	634	1 VC09_VACCC	P21042 vaccinia vi
5	42	75.0	634	1 VC09_VACCV	P17372 vaccinia vi
6	41	73.2	142	1 YPBH_KLEPN	P20775 klebsiella
7	41	73.2	257	1 YPB3_YEAST	P38195 saccharomyc
8	40	71.4	859	1 OSH1_YEAST	P35845 saccharomyc
9	40	71.4	1082	1 SP23_YEAST	P35210 saccharomyc
10	40	71.4	1154	1 VGL2_IBVD2	P12722 avian infec
11	40	71.4	1163	1 VGL2_IBV6	P05135 avian infec
12	40	71.4	1293	1 XPC_DROME	Q24595 drosophila
13	40	71.4	2452	1 RPB1_PLAFD	P14248 plasmodium
14	39.5	70.5	844	1 PBPB_ECOLI	P02919 e penicilli
15	39	69.6	194	1 YPBH_BACSU	P501937 mus musculi
16	39	69.6	292	1 NPM_MOUSE	P13084 rattus norv
17	39	69.6	292	1 NPM_MOUSE	P06748 homo sapien
18	39	69.6	294	1 NPM_MOUSE	Q09378 caenorhabdi
19	39	69.6	405	1 YS63_CAEEL	P05522 persea amer
20	39	69.6	494	1 GUN1_PERRA	P48201 haemophilus
21	39	69.6	707	1 YG31_YEAST	P48201 haemophilus
22	38	67.9	317	1 YG31_YEAST	P48201 haemophilus
23	38	67.9	441	1 YB66_YEAST	P38195 saccharomyc
24	38	67.9	443	1 YB66_YEAST	P38195 saccharomyc
25	38	67.9	1094	1 YB00_YEAST	P38195 saccharomyc
26	38	67.9	1345	1 YH00_YEAST	P38195 saccharomyc
27	38	67.9	1501	1 YH00_YEAST	P38195 saccharomyc
28	37	66.1	218	1 UBC8_CANAL	O45690 candida alb
29	37	66.1	264	1 T2D7_HUMAN	O16594 homo sapien
30	37	66.1	344	1 Y182_ARCFU	O30055 archaeoglob
31	37	66.1	373	1 YR14_YEAST	P43603 saccharomyc
32	37	66.1	391	1 NPL1_HUMAN	P55209 homo sapien
33	37	66.1	391	1 NPL1_MOUSE	P28656 mus musculi

34	37	66.1	395	1 SDC_DROME	P49415 drosophila
35	37	66.1	501	1 K63H_DROME	P83101 drosophila
36	37	66.1	595	1 SNX9_HUMAN	O95511 homo sapien
37	37	66.1	631	1 MERA_BACSR	P16171 bacillus sp
38	37	66.1	669	1 FPS1_YEAST	P23900 saccharomyc
39	37	66.1	700	1 CHE60_PLAFG	P34940 plasmodium
40	37	66.1	906	1 YPGL_DICSP	P10511 dictyosteli
41	37	66.1	1872	1 T2D1_HUMAN	P21675 homo sapien
42	37	66.1	1956	1 ARYL1_PLAFR	Q04956 plasmodium
43	37	66.1	2316	1 PTP2_RAT	Q62656 rattus norv
44	37	66.1	2411	1 DAB_DROME	P98081 drosophila
45	36.5	65.2	138	1 Y370_TREPA	O83385 treponema p

ALIGNMENTS

RESULT 1
ID K6P2_KLUOLA STANDARD: PRT; 957 AA.
AC Q03216;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 6-phosphofructokinase beta subunit (Pc 2.7.1.11) (Phosphofructokinase
1) (Phosphohexokinase) (6PF-1-K beta subunit).
GN PFK2.
OS Kluveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93316853; PubMed=8326866;
RA Heinisch J., Kirchbach L., Liesen T., Vogelsang K.,
RA Hollenberg C.P.;
RT "Molecular genetics of phosphofructokinase in the yeast Kluveromyces
lactis.";
RT Mol. Microbiol. 8:559-570(1993).
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
fructose 1,6-bisphosphate.
CC -1- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
CC -1- SUBUNIT: HETEROCTAMER OF 4 ALPHA AND 4 BETA CHAINS.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY. TWO DOMAIN
SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL: Z17316; CAA78964.1; -
DR PIR: S29603; S29603.
DR PIR: S32903; S32903.
DR HSRP: P00512; 3PK.
DR InterPro: IPR000023; Phosphofructokinase.
DR Pfam: PF00365; PFK_3.
DR PRINTS: PR00476; PHEPCKINASE.
DR PRODOM: PD000707; Phosphofructokinase.
DR PROSITE: PS00433; PHOSPHOFRUCTOKINASE; 2.
KW Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme;
KW Phosphorylation; Magnesium.
SQ SEQUENCE 957 AA; 104988 MW; 324483DB02E26C68 CRC64;

Query Match 80.4%; Score 45; DB 1; Length 957;
Best Local Similarity 87.5%; Pred. NO. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 DDDDYDFD 8

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:19 ; Search time 194.32 Seconds
(without alignments)
8.012 Million cell updates/sec

Title: US-09-780-035-28_COPY_89_97

Perfect score: 56

Sequence: 1 DDDDDYDPDY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP virus: *
16: SP bacteriophage: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	85.7	1578	16	Q92E25
2	46	82.1	1186	5	Q21227
3	46	82.1	1188	5	Q62302
4	44	78.6	921	5	Q969A3
5	43	76.8	380	10	Q91V94
6	43	76.8	492	5	Q9N1N9
7	43	76.8	625	12	Q9N1N8
8	43	76.8	630	12	Q9QCP6
9	43	76.8	708	10	Q98WQ0
10	43	75.9	356	12	Q9FZG1
11	42.5	75.0	51	16	Q923B6
12	42	75.0	51	16	Q9P1P4
13	42	75.0	440	10	Q941N4
14	42	75.0	689	5	Q97258
15	42	75.0	771	12	Q41111
16	42	75.0	1683	13	Q91741

17	42	75.0	4550	5	077336	077336 plasmodium
18	41.5	74.1	206	10	Q9SMP7	Q9SMP7 arabidopsis
19	41	73.2	235	5	076542	076542 dictyosteli
20	41	73.2	274	3	Q9P6X3	Q9P6X3 neurospora
21	41	73.2	391	5	Q26258	Q26258 chironomus
22	41	73.2	495	5	001422	001422 caenorhabd
23	41	73.2	498	10	Q94BM0	Q94BM0 hordeum vul
24	41	73.2	506	10	Q91G05	Q91G05 arabidopsis
25	41	73.2	561	5	Q19293	Q19293 caenorhabd
26	41	73.2	613	11	Q9CX13	Q9CX13 mus musculu
27	41	73.2	613	11	Q9JJA6	Q9JJA6 mus musculu
28	41	73.2	625	12	Q9E128	Q9E128 avian infec
29	41	73.2	626	5	P90922	P90922 caenorhabd
30	41	73.2	630	12	Q991L9	Q991L9 avian infec
31	41	73.2	634	12	Q9JFG8	Q9JFG8 vaccinia vi
32	41	73.2	804	10	Q9LXB6	Q9LXB6 arabidopsis
33	41	73.2	806	4	Q9H9X8	Q9H9X8 homo sapien
34	41	73.2	1103	4	Q9UHV3	Q9UHV3 homo sapien
35	41	73.2	1166	12	Q82666	Q82666 avian infec
36	41	73.2	1609	4	Q9P212	Q9P212 homo sapien
37	41	73.2	1717	10	Q94BM1	Q94BM1 hordeum vul
38	41	73.2	1720	10	Q94BM2	Q94BM2 hordeum vul
39	41	73.2	1994	4	Q9HC53	Q9HC53 homo sapien
40	41	73.2	2281	11	Q99P84	Q99P84 rattus norv
41	40	73.2	2303	4	Q9H9X6	Q9H9X6 homo sapien
42	40	71.4	111	16	Q92MB6	Q92MB6 rhizobium m
43	40	71.4	183	5	Q9VDB0	Q9VDB0 dirosophila
44	40	71.4	217	10	Q9LX99	Q9LX99 arabidopsis
45	40	71.4	319	10	Q9AWV3	Q9AWV3 oryza sativ

ALIGNMENTS

RESULT 1
ID Q92E25 PRELIMINARY; PRT; 1578 AA.
AC Q92E25;
DT 01-DEC-2001 (TREMUREL. 19, Created)
DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)
DE 01-DEC-2001 (TREMUREL. 19, Last annotation update)
DE PEPTIDOGLYCAN BOUND PROTEIN (LPXTG MOTIF) SIMILAR TO ADHESIN.
GN L1N0636.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Franquet L., Buchrieser C., Rusnick C., Amend A.,
BAguero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Ertian K.-D., Esihl H., Garcia-del Portillo F., Garrido P.,
GAutier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurpik G.,
RAMadueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluerter T., Simoes N., Tierrez A.,
RA Vaquer-Boland J.-A., Voss H., Weiland J., Cossart P.,
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL: AL596165; CAC95868.1; -
DR ListList: L1N0636; -
KW Complete proteome.
SQ SEQUENCE 1578 AA; 172708 MW; BA7576778EED709 CMC64;

Query Match 85.7%; Score 48; DB 16; Length 1578;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DDDDYDEFDY 9
1:1:1:1:1:1
Db 620 DEDDFDFDY 628

RESULT 2
ID 021227 PRELIMINARY; PRT; 1186 AA.
AC 021227;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-2000 (TREMBlrel. 13, Last annotation update)
DE K04G2.8A PROTEIN.
GN APR-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RA SEQUENCE FROM N.A.
RA Gardner A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL;
RX MEDLINE-97433081; PubMed-9288750;
RA Rochelleau C.E., Downs W.D., Lin R., Wiltmann C., Bel Y., Cha Y.-H.,
RT All M., Priess J.R., Mello C.C.;
RT "Wnt signaling and an APC-related gene specify endoderm in early C.
elegans embryos."
RL Cell 90:707-716(1997).
DR EMBL; 275712; CAB00045.1;
DR EMBL; AF013950; AAC47747.1;
SQ SEQUENCE 1186 AA; 131713 MW; CBE672D78E2B245D CRC64;

Query Match 82.1%; Score 46; DB 5; Length 1186;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DDDDYDEFDY 9
1:1:1:1:1:1
Db 964 DDDDYDYTY 972

RESULT 3
ID 062302 PRELIMINARY; PRT; 1188 AA.
AC 062302;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE K04G2.8B PROTEIN.
GN K04G2.8B.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RA SEQUENCE FROM N.A.
RA Gardner A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE-99069613; PubMed-9851916;
RA none;
RT "Investigating biology."
RT Science 282:2012-2018(1998).
DR EMBL; 275712; CAB00048.1;
SQ SEQUENCE 1188 AA; 131989 MW; F3CDA53B5D3527A0 CRC64;

Query Match 82.1%; Score 46; DB 5; Length 1188;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DDDDYDEFDY 9
1:1:1:1:1:1
Db 966 DDDDYDYTY 974

RESULT 4
ID 0969A3 PRELIMINARY; PRT; 921 AA.
AC 0969A3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE COMPLEMENT COMPONENT C6.
GN AMPHIC6.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RA Suzuki M.M., Satoh N., Nonaka M.;
RT "Complement Components C3 and C6 from Amphioxus."
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB050669; BAB47147.1;
SQ SEQUENCE 921 AA; 99659 MW; 9731CF5A0DB508 CRC64;

Query Match 78.6%; Score 44; DB 5; Length 921;
Best Local Similarity 77.8%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DDDDYDEFDY 9
1:1:1:1:1:1
Db 913 DDDDYDYTY 921

RESULT 5
ID 09LV94 PRELIMINARY; PRT; 380 AA.
AC 09LV94;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SIMILARITY TO UNKNOWN PROTEIN (AT5G64830/MX3_5).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE-20181125; PubMed-10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
features of the regions of 3,076,755 bp covered by sixty P1 and TAC
clones."
RT DNA Res. 7:31-63(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Iwadi J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:46 ; Search time 84.18 seconds

(without alignments)
2.611 Million cell updates/sec

Title: US-09-780-035-28_COPY_89_97
Perfect score: 56
Sequence: 1 DDDYDFDY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCROS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	78.6	1417	2	US-08-559-303B-78
2	44	78.6	1417	3	US-08-781-891-78
3	44	78.6	1417	4	US-09-175-828-78
4	43	76.8	492	4	US-08-845-258-21
5	43	76.8	492	4	US-08-990-571-21
6	43	76.8	492	4	US-08-723-142A-21
7	43	76.8	503	4	US-08-845-258-52
8	43	76.8	503	4	US-08-990-571-52
9	40	71.4	700	2	US-08-568-459A-10
10	40	71.4	700	2	US-08-487-826B-10
11	40	71.4	705	2	US-08-663-556A-19
12	40	71.4	705	2	US-08-023-610-19
13	40	71.4	705	2	US-08-288-065A-19
14	40	71.4	705	2	US-08-362-240A-19
15	40	71.4	705	2	PCT-US95-10245-19
16	40	71.4	2182	2	US-08-487-826B-16
17	39.5	70.5	532	3	US-08-481-435-12
18	39.5	70.5	532	3	US-08-481-435-11
19	39.5	70.5	823	3	US-08-481-435-4
20	39.5	70.5	836	3	US-08-481-435-9
21	39.5	70.5	844	3	US-08-481-435-7
22	39.5	70.5	844	3	US-08-481-435-8
23	39.5	70.5	257	4	US-09-538-871-4
24	39	69.6	292	4	US-09-538-871-2
25	39	69.6	494	4	US-09-006-636-8
26	39	69.6	494	4	US-09-006-632-8
27	38	67.9	383	2	US-08-484-575A-4

28	38	67.9	383	3	US-08-477-459-4	Sequence 4, Appl1
29	38	67.9	383	3	US-08-479-869-4	Sequence 4, Appl1
30	38	67.9	383	4	US-08-486-414-4	Sequence 4, Appl1
31	38	67.9	383	5	PCT-US94-01826A-4	Sequence 4, Appl1
32	38	67.9	383	5	PCT-US94-02252A-4	Sequence 4, Appl1
33	37	66.1	264	1	US-08-188-582-26	Sequence 26, Appl
34	37	66.1	264	1	US-08-646-715-26	Sequence 26, Appl
35	37	66.1	545	3	US-08-974-180-15	Sequence 15, Appl
36	37	66.1	783	6	5231168-2	Patent No. 5231168
37	37	66.1	1042	3	US-08-928-361B-11	Sequence 11, Appl
38	37	66.1	1043	3	US-08-928-361B-30	Sequence 30, Appl
39	37	66.1	1721	3	US-08-700-651-5	Sequence 5, Appl1
40	37	66.1	1721	3	US-08-928-361B-6	Sequence 6, Appl1
41	37	66.1	1837	3	US-08-928-361B-5	Sequence 5, Appl1
42	37	66.1	1872	1	US-08-188-582-14	Sequence 14, Appl
43	37	66.1	1872	1	US-08-646-715-14	Sequence 14, Appl
44	37	66.1	1893	1	US-08-188-582-11	Sequence 11, Appl
45	37	66.1	1893	1	US-08-646-715-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-559-303B-78
Sequence 78, Application US/08559303B
Patent No. 5824501
GENERAL INFORMATION:
APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
APPLICANT: GRODEN
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT
OF BLOOM'S SYNDROME
TITLE OF INVENTION: OF BLOOM'S SYNDROME
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESSES:
ADDRESSEE: AMSTER, ROTHSTEIN & EBBNSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,303B
FILING DATE: NOVEMBER 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 1417
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: OTHER NUCLEIC ACID
DESCRIPTION: YES
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-559-303B-78

Query Match 78.6%; Score 44; DB 2; Length 1417;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DDDDYDFDY 9
11111111
DB 292 DDDDYDTDF 300

RESULT 2

US-08-781-891-78
; Sequence 78, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: FU, Yang-Hui
; APPLICANT: YU, Chang-Hu
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620Leuburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1417 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-781-891-78

Query Match 78.6%; Score 44; DB 3; Length 1417;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DDDDYDFDY 9
11111111
DB 292 DDDDYDTDF 300

RESULT 3

US-09-175-828-78
; Sequence 78, Application US/09175828
; Patent No. 6221643
; GENERAL INFORMATION:
; APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
; APPLICANT: GRODEN
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT
; TITLE OF INVENTION: OF BLOOM'S SYNDROME

NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/175,828

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/559,303

FILING DATE: NOVEMBER 15, 1995

ATTORNEY/AGENT INFORMATION:

NAME: ELIZABETH A. BOGOSIAN

REGISTRATION NUMBER: 39,911

REFERENCE/DOCKET NUMBER: 63475/65

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 697-5995

TELEFAX: (212) 286-0854 or 286-0082

TELEX: TWX 710-581-4766

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 1417

TYPE: AMINO ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE:

DESCRIPTION: OTHER NUCLEIC ACID

HYPOTHETICAL: YES

ANTI-SENSE: NO

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-09-175-828-78

Query Match 78.6%; Score 44; DB 4; Length 1417;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DDDDYDFDY 9
11111111
DB 292 DDDDYDTDF 300

RESULT 4

US-08-845-258-21
; Sequence 21, Application US/08845258
; Patent No. 6183976
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:17 ; Search time 245.49 Seconds
(without alignments)
5.882 Million cell updates/sec

Title: US-09-780-035-29_COPY_23_35
Sequence: 1 SGSSSNGINAVN 13

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
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- 11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
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- 14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
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- 19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	13	22	AA65313
2	62	100.0	111	22	AA65319
3	62	100.0	111	22	AA65355
4	62	100.0	235	22	AA65320
5	55	88.7	98	21	AA640145
6	55	88.7	111	18	AA613519
7	55	88.7	119	22	ABB31633
8	55	88.7	119	22	ABB2173
9	55	88.7	119	22	AA66997
10	55	88.7	353	22	ABG26353
11	53	85.5	111	17	AA88506

12	52	83.9	13	20	AA690302	Human anti-GPIIb/IIIa
13	52	83.9	98	21	AA640144	Anti-IL12 antibody
14	52	83.9	109	22	AA693613	Human anti-Rh(D) c
15	52	83.9	110	22	AA690281	Anti-adipocyte mon
16	52	83.9	111	20	AA690281	Human anti-GPIIb/IIIa
17	52	83.9	111	22	AA662955	Amino acid sequenc
18	52	83.9	118	22	AA665555	Amino acid sequenc
19	52	83.9	132	22	AA665555	Amino acid sequenc
20	52	83.9	237	22	AA619300	Novel human diapo
21	52	83.9	240	22	AA646050	Human TF anti-idio
22	52	83.9	244	22	AA646050	Human TF anti-idio
23	51	82.3	76	20	AA612696	Human 5' EST seque
24	51	82.3	109	22	AA693614	Human anti-Rh(D) c
25	51	82.3	241	22	AA646051	Human TF anti-idio
26	50	80.6	250	22	AA626352	Novel human diapo
27	50	80.6	250	22	AA619301	Novel human diapo
28	48	77.4	126	22	AA626350	Novel human diapo
29	47	75.8	13	22	AA666403	Anti-TANGO 268 scF
30	45	72.6	109	18	AA627547	Human Ab light cha
31	45	72.6	118	22	AA680208	Human autoantibody
32	45	72.6	153	21	AA653653	Human colon cancer
33	44	71.0	13	21	AA65206	Anti-platelet glyco
34	44	71.0	98	21	AA640142	Human anti-Rh(D) c
35	44	71.0	98	21	AA640142	Human anti-Rh(D) c
36	44	71.0	98	21	AA640145	Anti-IL12 antibody
37	44	71.0	109	14	AA68606	KOL light chain.
38	44	71.0	109	21	AA695204	Anti-platelet glyco
39	44	71.0	109	21	AA695205	Human anti-Rh(D) c
40	44	71.0	109	22	AA693612	Human anti-Rh(D) c
41	44	71.0	109	22	AA693616	Human anti-Rh(D) c
42	44	71.0	110	21	AA695182	Anti-platelet glyco
43	44	71.0	110	22	AA693617	Human anti-Rh(D) c
44	44	71.0	111	14	AA68607	KOL light chain.
45	44	71.0	111	18	AA613528	Anti-melanoma ligh

ALIGNMENTS

RESULT 1	AA65313	standard; protein; 13 AA.
ID	AA65313	
AC	AA65313	
DT	30-NOV-2001	(first entry)
DE	Anti-IL-18 antibody LTR28 light chain CDRL fragment.	
KW	IL-18; interleukin-18; human; antibody; antineoplastic; cerebroprotective; noctropic; neurological; antiinflammatory; antiparkinsonian; cardiant; immunosuppressive; antidepressant; neuroleptic; hepatotropic; LTR28.	
KW	Homo sapiens.	
OS	Homo sapiens.	
PN	W0200158956-A2.	
XX	16-AUG-2001.	
XX	09-FEB-2001; 2001WO-US04170.	
XX	10-FEB-2000; 2000US-0181608.	
PA	(BADI) BASF AG.	
PI	Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;	
PI	Duncan AR, Brocklehurst SM, Mankovich J, Shorrocks CP, Thompson JB;	
PI	Lennard SN;	
DR	WPI: 2001-550020/61.	
XX	Novel antibodies and compounds capable of binding to human	
PT	interleukin-18 useful for treating, e.g., inflammatory disorders,	

PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Claim 34; Page 42; 91pp; English.
 XX
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LT28
 CC light chain CDRL fragment.
 XX
 SQ Sequence 13 AA;
 XX
 Query Match 100.0%; Score 62; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00073;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSSSNIGINAVN 13
 DB 1 sgsssnlglnavn 13
 IIIIIIIIIIII
 RESULT 2
 ID AAG65319 standard; protein; 111 AA.
 XX
 AC AAG65319;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Anti-IL-18 antibody LT28 light chain sequence.
 XX
 IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADT) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI: 2001-550020/61.
 DR N-PSDB; AAH47514.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Claim 36; Page 42; 91pp; English.

XX
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LT28
 CC light chain sequence.
 XX
 SQ Sequence 111 AA;
 XX
 Query Match 100.0%; Score 62; DB 22; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSSSNIGINAVN 13
 DB 23 sgsssnlglnavn 35
 IIIIIIIIIIII
 RESULT 3
 ID AAG65355 standard; protein; 111 AA.
 XX
 AC AAG65355;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Anti-IL-18 antibody LT28 light chain sequence.
 XX
 IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADT) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI: 2001-550020/61.
 DR N-PSDB; AAH47514.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Example 2; Page 90; 91pp; English.
 XX
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a

CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LRT8
 CC light chain sequence.

XX Sequence 111 AA;

Query Match 100.0%; Score 62; DB 22; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSSSNIGINAVN 13
 Db 23 sgsssniglnavn 35

RESULT 4
 AAG65320
 ID AAG65320 standard; protein; 235 AA.

XX AAG65320;

XX 30-NOV-2001 (first entry)

DE Anti-IL-18 antibody LRT8 sequence.

XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KM neoptotic; neurological; antiinflammatory; antiparisonian; cardiant;
 KM immunosuppressive; antidepressant; neuroleptic; hepatotropic; LRT8.

XX Homo sapiens.

XX WO200158956-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04170.

XX 10-FEB-2000; 2000US-0181608.

XX (BADI) BASF AG.

XX Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrocks CP, Thompson JE;
 PI Leonard SN;

XX WPI; 2001-550020/61.

XX Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -

XX Examples; Page 79-80; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such

CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LRT8
 CC comprising the heavy chain and light chain sequences joined by a linker.
 XX Sequence 235 AA;

Query Match 100.0%; Score 62; DB 22; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSSSNIGINAVN 13
 Db 147 sgsssniglnavn 159

RESULT 5
 AAB40146
 ID AAB40146 standard; Protein; 98 AA.

XX AAB40146;

XX 05-FEB-2001 (first entry)

DE Anti-hIL12 antibody L chain V region amino acid sequence SEQ ID 672.

XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KM complementarity determining region; CDR; antirheumatic; antiarthritic;
 KM antisclerotic; neuroprotective; antipsoriatic; antiaesthetic; cardiant;
 KM antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KM multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

XX WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US07946.

XX 25-MAR-1999; 99US-0126603.

XX (BADI) BASF AG.

XX (GEMV) GENETICS INST INC.

XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to

PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's

PT disease and multiple sclerosis -

XX Claim 75; Page 123; 377pp; English.

XX This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and

CC construction of the antibodies of the invention are given in
 CC AAC1062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antitumoural; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antiparasitic; antischistosomal;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.

CC Sequence 98 AA:

Query Match 88.7%; Score 55; DB 21; Length 98;
 Best Local Similarity 92.3%; Pred. No. 0.081; 1; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSSSNNIGINAVN 13
 Db 23 ssssnignavn 35

RESULT 6
 AAW13519
 ID AAW13519 standard; protein; 111 AA.

AC AAW13519;

DT 28-OCT-1997 (first entry)

DE Anti-melanoma light chain antibody clone Z78.

KW Human; monoclonal antitumour antibody; peripheral blood lymphocyte;

KW cancer; tumorigenesis; anticancer vaccine.

OS Homo sapiens.

Key Location/Qualifiers

FT Region 23..35 /label= CDR1

FT Region 51..57 /label= CDR2

FT Region 90..99 /label= CDR3

PN WO9702479-A2.

PD 23-JAN-1997.

PF 28-JUN-1996; 96WO-IB01032.

PR 30-JUN-1995; 95US-0497647.

PA (UYVA) UNIV YALE.

PI Cal X, Garen A;

DR WPI; 1997-109061/10.

PT Prodn. of human monoclonal anti-tumour antibodies - by screening a
 PT fusion phase library produced using peripheral blood lymphocytes
 PT from a cancer patient

PS Claim 19; Page 57; 82pp; English.

CC A process for isolating and synthesising human monoclonal anti-tumour
 CC antibodies has been produced. The process involves: (a) constructing at
 CC least one fusion phase library from the peripheral blood lymphocytes
 CC (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in
 CC the phase library in a binding assay with cultured tumour cells of the
 CC same type as the patient's tumour; (c) removing extraneous antibodies by
 CC absorption against normal human cells; (d) cloning the phase selected in

CC step (b) and (c); (e) assaying the specificity of the cloned phage by
 CC incubating the phage with at least two types of cultured normal cells;
 CC and (f) further testing the specificity of cloned phage that do not bind
 CC to either cell line of cultured normal cells in further binding assays
 CC to cultured tumour cells derived from more than one other tumour that is
 CC not the patient's tumour. The present sequence represents a human light
 CC chain antibody, from an scFv antibody fusion phage library, produced by
 CC a method as described above. The antibodies produced can be used for
 CC diagnostic and therapeutic applications and for isolating tumour
 CC antigens for studying tumorigenesis or for use as anti-cancer vaccines.
 CC The human antibodies have low immunogenicity in humans compared to
 CC murine monoclonal antibodies (Mabs). Since the antibodies are isolated
 CC from fusion phage libraries, their affinity and specificity for a
 CC tumour cell line can be improved by genetic manipulations.

CC Sequence 111 AA;

Query Match 88.7%; Score 55; DB 18; Length 111;
 Best Local Similarity 92.3%; Pred. No. 0.092; 1; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSSSNNIGINAVN 13
 Db 23 ssssnignavn 35

RESULT 7
 ABB31633
 ID ABB31633 standard; Peptide; 119 AA.

AC ABB31633;

DT 01-FEB-2002 (first entry)

DE Peptide #4284 encoded by breast cell single exon nucleic acid probe.

KW Human; microarray; single exon probe; gene expression; breast;

KW disease; cancer.

OS Homo sapiens.

PN WO200157271-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00662.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-496933/54.

PT New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes

PS Claim 27; SEQ ID NO 14601; 327pp + sequence listing; English.

CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label

CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
xx
SQ Sequence 119 AA:

CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pat_sequences](http://wipo.int/pub/published_pat_sequences).

OY 1 SSSSSNIGINAVN 13
 DB 23 sssssnignavn 35

RESULT 10

ABG26353
 ID ABG26353 standard; Protein: 353 AA.

AC ABG26353;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #26344.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS90540.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS Claim 20; SEQ ID No 56712; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 353 AA;

Query Match 88.7%; Score 55; DB 22; Length 353;
 Best Local Similarity 92.3%; Pred. No. 0.3;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SSSSSNIGINAVN 13
 DB 187 sssssnignavn 199

RESULT 11

AAR88506
 ID AAR88506 standard; Protein: 111 AA.

AC AAR88506;

DT 31-JUL-1996 (first entry)

DE VLambda for antibody BT34/A5.

KW Antibody; variable light chain; VLambda; human; monoclonal; BT34/A5;
 BT32/A6; cell cycle independent; tumour specific; glioma; therapy; Mab;
 detection; complementarity determining region; CDR.

OS Homo sapiens.

PN WO9535374-A1.

PD 28-DEC-1995.

PF 16-JUN-1995; 95WO-CA00361.

PR 21-JUN-1994; 94US-0264093.

PA (DANM/) DAN M D.

PI Dan MD;

DR WPI; 1996-058411/06.

DR N-PSDB; AAT10940.

PT Novel monoclonal antibodies, BT34/A5 and BT32/A6 - used to
 PT characterise glioma specific cell surface antigens, and in the
 PT treatment of glioma

PS Claim 11; Page 34; 53pp; English.

CC AAR88504-R88510 represent regions of the human monoclonal antibodies
 CC (Mab's) BT34/A5 and BT32/A6. This sequence represents the variable
 CC region of the light chain, subgroup lambda, (VLambda) of BT34/A5. The
 CC complementarity determining regions (CDR's) of this sequence are
 CC specifically claimed. This sequence preferably has an N-terminal
 CC extension comprising the signal sequence represented by AAR88507. The
 CC BT34/A5 and BT32/A6 Mab's recognise a cell cycle independent tumour
 CC specific antigen. They also bind equally well to tumour cells in vitro
 CC regardless of their culture viability, growth characteristics, or
 CC culture density. The antibodies effectively label the tumour cells by
 CC binding to the antigen present on the cell surface. The Mab's are useful
 CC in the detection and the treatment of glioma. These Mab's are specific
 CC for glioma and show none of the cross-reactivity seen with previous
 CC antibodies.

XX Sequence 111 AA;

Query Match 85.5%; Score 53; DB 17; Length 111;
 Best Local Similarity 84.6%; Pred. No. 0.2;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSSSNGINAVN 13
 |||||
 DB 23 sgssnsgntvsn 35

RESULT 12

AAW90302
 ID AAW90302 standard; Protein; 13 AA.

AC AAW90302;

DT 07-SEP-1999 (first entry)

DE Human anti-GPIIb/IIIa auto-antibody light chain protein CDRI region 2.

XX Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
 KW blood platelet membrane protein; predisposition; prevention; treatment;
 KW autoimmune thrombocytopenic purpura; AITP; fibrinogen binding; thrombi;
 KW thrombocyte; cardiac infarction; pulmonary embolism; light chain.

OS Homo sapiens.

PN WO985619-A1.

PD 10-DEC-1998.

PF 05-JUN-1998; 98WO-EP03397.

PR 08-MAY-1998; 98DE-1020663.

PR 06-JUN-1997; 97DE-1023904.

PR 12-DEC-1997; 97DE-1055227.

PA (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.

PI Berchold P, Escher RFA;

DR WPI; 1999-105496/09.

PT Nucleic acid encoding human autoantibodies against platelet
 glycoprotein IIb/IIIa - used for diagnosis, treatment and prevention
 of autoimmune thrombocytopenic purpura and for modulation of
 fibrinogen binding

PS Claim 5b; Page 6; 93pp; German.

CC This invention describes novel nucleic acid fragments that encode human
 CC auto-antibodies and anti-idiotypic antibodies against blood platelet
 CC membrane protein, GPIIb/IIIa. The products of the invention are used
 CC for diagnosis (including monitoring and determining predisposition),
 CC prevention and treatment of autoimmune thrombocytopenic purpura (AITP)
 CC (particularly to dissolve thrombi and/or prevent their formation, e.g.
 CC in cases of cardiac infarction or pulmonary embolism). Unlike murine
 CC antibodies, human antibodies (hAb) do not induce adverse side effects
 CC and persist for longer in vivo than small peptides. AAW90293-W90337
 CC represent antibody fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 83.9%; Score 52; DB 20; Length 13;

Best Local Similarity 84.6%; Pred. No. 0.032;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSSSNGINAVN 13
 |||||
 DB 1 sgssnsgntvsn 13

RESULT 13
 AAB40144

ID AAB40144 standard; Protein; 98 AA.
 XX AAB40144;
 AC AAB40144;
 XX AAB40144;
 DT 05-FEB-2001 (first entry)

DE Anti-IL12 antibody L chain V region amino acid sequence SEQ ID 670.

XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarily determining region; CDR; antineumatic; antiarthritic;
 KW antisclerotic; neutroprotective; antiparastitic; antisclerotic; cardiant;
 KW antiparastitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

PN WO200056772-A1.

PD 28-SEP-2000.

PF 24-MAR-2000; 2000WO-US07946.

PR 25-MAR-1999; 99US-0126603.

PA (BADT) BASF AG.
 (GEMY) GENETICS INST INC.

PI Salfield JG, Roguska M, Banerjee S, Tracey DE, White M;
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Werne NW, Widom A, Elyan JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 DR WPI; 2000-638250/61.

PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -

PS Claim 75; Page 123; 377pp; English.

CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarily determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAB61062-C61071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neutroprotective; antiparastitic; antisclerotic;
 CC cardiant; antiparastitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.

XX Sequence 98 AA;

Query Match 83.9%; Score 52; DB 21; Length 98;

Best Local Similarity 84.6%; Pred. No. 0.25;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSSSNGINAVN 13
 |||||
 DB 23 sgssnsgntvsn 35

RESULT 14
 AAG93613
 ID AAG93613 standard; Protein; 109 AA.
 XX
 AC AAG93613;
 XX
 DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) chain L04 protein sequence.
 XX
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 XX
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US625455-B1.
 XX
 PD 03-JUL-2001.
 XX
 PE 29-JAN-1999; 99US-0240274.
 XX
 PF 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNITV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR WPI; 2001-388931/41.
 DR N-PSDB; AAH68670.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 XX
 PS Claim 1; Column 45; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (1) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH66615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 CC
 XX
 SQ Sequence 109 AA;
 XX
 QY Query Match 83.9%; Score 52; DB 22; Length 109;
 Best Local Similarity 84.6%; Pred. No. 0.28; 2; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 2;
 XX
 DB 1 SGSSNIGINAVN 13
 22 sgssnignntvn 34
 XX
 RESULT 15
 AAU02618
 ID AAU02618 standard; Protein; 110 AA.
 XX
 AC AAU02618;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Anti-adipocyte monoclonal antibody light chain, FAT 105.
 XX
 KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;

KW heart disease; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 WO200127279-A1.
 XX
 XX
 PD 19-APR-2001.
 XX
 PE 11-OCT-2000; 2000WO-GB03900.
 XX
 PF 12-OCT-1999; 99US-0158812.
 PR
 PR (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PA Edwards BM, Main SH, Vaughan TJ;
 XX
 PI
 DR WPI; 2001-282031/29.
 DR N-PSDB; AAS03518.
 XX
 PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity
 PT related diseases -
 XX
 PS Claim 1; Page 166; 182pp; English.
 XX
 CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
 CC chain, and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease.
 CC
 XX
 SQ Sequence 110 AA;
 XX
 QY Query Match 83.9%; Score 52; DB 22; Length 110;
 Best Local Similarity 84.6%; Pred. No. 0.28;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 DB 1 SGSSNIGINAVN 13
 23 sgssnignntvn 35
 XX

Search completed: June 21, 2002, 09:20:18
 Job time: 431 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:48 ; Search time 84.18 Seconds
(without alignments)
3.772 Million cell updates/sec

Title: US-09-780-035-29_COPY_23_35
Perfect score: 62
Sequence: 1 SGSSNIGINAVN 13

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	88.7	113	4	US-08-983-607-27
2	53	85.5	13	1	US-08-264-093-18
3	53	85.5	111	1	US-08-264-093-6
4	52	83.9	109	4	US-09-240-274-56
5	51	82.3	109	4	US-09-240-274-57
6	45	72.6	109	4	US-09-025-769B-32
7	45	72.6	109	4	US-09-025-769B-51
8	44	71.0	98	1	US-08-211-202-111
9	44	71.0	98	2	US-08-665-202-37
10	44	71.0	98	2	US-08-665-202-38
11	44	71.0	109	4	US-09-240-274-55
12	44	71.0	109	4	US-09-240-274-59
13	44	71.0	110	1	US-07-942-245-26
14	44	71.0	110	1	US-09-240-274-60
15	44	71.0	111	1	US-08-107-669D-4
16	44	71.0	111	1	US-08-472-788A-4
17	44	71.0	111	2	US-08-477-531B-4
18	44	71.0	111	2	US-08-082-842A-4
19	44	71.0	111	2	US-08-665-202-36
20	44	71.0	111	2	US-08-665-202-42
21	44	71.0	111	2	US-08-665-202-43
22	44	71.0	111	4	US-08-983-607-21
23	44	71.0	111	4	US-08-983-607-23
24	44	71.0	111	4	US-08-983-607-35
25	44	71.0	112	2	US-08-665-202-39
26	44	71.0	112	2	US-08-983-607-31
27	44	71.0	112	4	US-09-025-769B-18

28	44	71.0	113	1	US-08-211-202-113	Sequence 113, App
29	44	71.0	113	1	US-08-211-202-114	Sequence 114, App
30	44	71.0	114	4	US-09-240-274-62	Sequence 62, App1
31	44	71.0	258	2	US-08-665-202-5	Sequence 5, App1
32	44	71.0	282	4	US-09-420-592A-7	Sequence 7, App1
33	43	69.4	113	1	US-08-211-202-112	Sequence 112, App
34	42	67.7	109	4	US-09-240-274-54	Sequence 54, App1
35	41	66.1	104	2	US-08-273-146-63	Sequence 63, App1
36	41	66.1	110	2	US-08-199-911-2	Sequence 2, App1
37	39	62.9	111	2	US-08-665-202-41	Sequence 41, App1
38	38	61.3	109	4	US-09-240-274-61	Sequence 61, App1
39	38	61.3	109	4	US-09-240-274-180	Sequence 180, App
40	38	61.3	111	2	US-08-665-202-40	Sequence 40, App1
41	38	61.3	347	4	US-08-965-762-23	Sequence 23, App1
42	37	59.7	112	1	US-07-942-245-6	Sequence 6, App1
43	36	58.1	111	2	US-08-652-816A-15	Sequence 15, App1
44	36	58.1	235	4	US-09-049-672A-12	Sequence 12, App1
45	36	58.1	424	2	US-08-871-268A-23	Sequence 23, App1

ALIGNMENTS

RESULT 1
US-08-983-607-27
Sequence 27, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Department of Molecular Biophysics
and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes

IMMEDIATE SOURCE:
LIBRARY: DMA14 scfv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: 278
FEATURE:
NAME/KEY: light chain
US-08-983-607-27

Query Match 88.7%; Score 53; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.029;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSSSSNIGINAVN 13
DB 23 SSSSSNIGINAVN 35

RESULT 2
US-08-264-093-18
Sequence 18, Application US/08264093
Patent No. 5639863

GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-18

Query Match 85.5%; Score 53; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 0.0064;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSSSNIGINAVN 13
DB 1 SSSSSNIGTNTVN 13

RESULT 3
US-08-264-093-6

Sequence 6, Application US/08264093
Patent No. 5639863

GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-6

Query Match 85.5%; Score 53; DB 1; Length 111;
Best Local Similarity 84.6%; Pred. No. 0.061;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSSSNIGINAVN 13
DB 23 SSSSSNIGTNTVN 35

RESULT 4
US-09-240-274-56
Sequence 56, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

OTHER INFORMATION: anti-Rh(D) chain L04
US-09-240-274-56

Query Match 83.9%; Score 52; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.087;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SGSSSNGINAVN 13
Db 22 SGSSSNGISNTVN 34

RESULT 5
US-09-240-274-57
Sequence 57, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain L05
US-09-240-274-57

Query Match 82.3%; Score 51; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SGSSSNGINAVN 13
Db 22 SGSSSNGISNTVN 34

RESULT 6
US-09-025-769B-32
Sequence 32, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-32

Query Match 72.6%; Score 45; DB 4; Length 109;
Best Local Similarity 76.9%; Pred. No. 1.2;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SGSSSNGINAVN 13
Db 23 SGSSSNGISNTVS 35

RESULT 7
US-09-025-769B-51
Sequence 51, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-51

Query Match 72.6%; Score 45; DB 4; Length 109;
Best Local Similarity 76.9%; Pred. No. 1.2;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSSNGINAVN 13
||||||| |
Db 23 SSSSNGINAVS 35

RESULT 8
US-08-211-202-111
; Sequence 11, Application US/08211202
; Patent No. 5565332

GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Mattheus
APPLICANT: BAUER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211.202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-211-202-111

Query Match 71.0%; Score 44; DB 1; Length 98;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSSNGINAV 12
||||||| |
Db 23 SSSSNGINAV 34

RESULT 9
US-08-665-202-37
; Sequence 37, Application US/08665202
; Patent No. 5977322

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-37

Query Match 71.0%; Score 44; DB 2; Length 98;
Best Local Similarity 76.9%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSSNGINAVN 13
||||||| |
Db 23 SSSSNGINAVS 35

RESULT 10
US-08-665-202-38
; Sequence 38, Application US/08665202

Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schler, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-38

Query Match 71.0%; Score 44; DB 2; Length 98;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSSSNGINAV 12
|||||||
Db 23 SGSSSNGISNIV 34

RESULT 11
US-09-240-274-55
Sequence 55, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55

LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain I03
US-09-240-274-55

Query Match 71.0%; Score 44; DB 4; Length 109;
Best Local Similarity 76.9%; Pred. No. 1.7;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSSSNGINAVN 13
|||||||
Db 22 SGSSSNGISNHNVS 34

RESULT 12
US-09-240-274-59
Sequence 59, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain M02
US-09-240-274-59

Query Match 71.0%; Score 44; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSSSNGINAV 12
|||||||
Db 22 SGSSSNGISNIV 33

RESULT 13
US-07-942-245-26
Sequence 26, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: HP 9000/700 Workstation
 OPERATING SYSTEM: UNIX
 SOFTWARE: In house
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/942,245
 FILING DATE: 09-SEP-1992
 CLASSIFICATION: 530
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 TELEX: 6491103
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 110 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-07-942-245-26

Query Match 71.0%; Score 44; DB 1; Length 110;
 Best Local Similarity 69.2%; Pred. No. 1.7;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSSSNIGINAVN 13
 DB 23 SGTSSNIGSTVN 35

RESULT 14
 US-09-240-274-60
 Sequence 60, Application US/09240274
 Patent No. 6253455
 GENERAL INFORMATION:
 APPLICANT: Siegel, Donald L.
 TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 FILE REFERENCE: 09596-4202
 CURRENT APPLICATION NUMBER: US/09/240,274
 CURRENT FILING DATE: 1999-01-29
 EARLIER APPLICATION NUMBER: 60/081,380
 EARLIER FILING DATE: 1998-04-10
 EARLIER APPLICATION NUMBER: 60/028,550
 EARLIER FILING DATE: 1996-10-11
 NUMBER OF SEQ ID NOS: 224
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 60
 LENGTH: 110
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: anti-Rh(D) chain M03
 US-09-240-274-60

Query Match 71.0%; Score 44; DB 4; Length 110;
 Best Local Similarity 83.3%; Pred. No. 1.7;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSSSNIGINAV 12
 DB 22 SGSSSNIGSNYV 33

RESULT 15
 US-08-107-669D-4
 Sequence 4, Application US/08107669D
 Patent No. 5766886
 GENERAL INFORMATION:
 APPLICANT: Studnicka, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
 NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
 STREET: 1100 New York Ave., N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States of America
 ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/107,669D
 FILING DATE: 13-AUG-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/10906
 FILING DATE: 14-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/808,464
 FILING DATE: 13-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Michele A. Gambala
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/371-2600
 TELEFAX: 202/371-2540
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-107-669D-4

Query Match 71.0%; Score 44; DB 1; Length 111;
 Best Local Similarity 69.2%; Pred. No. 1.8;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSSSNIGINAVN 13
 DB 23 SGTSSNIGSTVN 35

Search completed: June 21, 2002, 09:21:48
 Job time: 411 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:43 ; Search time 109.39 Seconds

(without alignments)
11.419 Million cell updates/sec

Title: US-09-780-035-29_COPY_23_35

Perfect score: 62

Sequence: 1 SGSSSNIGINAVN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

PIR 71: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	88.7	98	2	Ig lambda chain -
2	53	85.5	112	2	Ig lambda chain V
3	53	85.5	112	2	Ig lambda chain V
4	52	83.9	98	2	Ig lambda chain -
5	52	83.9	112	2	Ig lambda chain V
6	52	83.9	117	2	Ig lambda chain V
7	52	83.9	233	2	Ig lambda chain -
8	50	80.6	112	2	Ig lambda chain V
9	50	80.6	112	2	Ig lambda chain V
10	49	79.0	234	2	Ig lambda chain -
11	48	77.4	110	2	Ig lambda chain V
12	47	75.8	149	2	Ig lambda chain V
13	46	74.2	110	2	Ig lambda chain V
14	46	74.2	216	2	Ig lambda chain V
15	44	71.0	95	2	Ig lambda chain -
16	44	71.0	98	2	Ig lambda chain -
17	44	71.0	98	2	Ig lambda chain -
18	44	71.0	109	1	Ig lambda chain -
19	44	71.0	111	1	Ig lambda chain V
20	44	71.0	111	1	Ig lambda chain V
21	44	71.0	111	2	Ig lambda chain V
22	44	71.0	111	2	Ig lambda chain V
23	44	71.0	113	2	Ig lambda chain V
24	44	71.0	129	2	Ig lambda chain V
25	44	71.0	130	2	Ig lambda chain pr
26	44	71.0	216	2	Ig lambda chain pr
27	44	71.0	232	2	Ig lambda chain (K
28	44	71.0	233	2	Ig lambda chain -
29	44	71.0	235	2	Ig lambda chain pr

30	42	67.7	235	2	S25750	Ig lambda chain -
31	41	66.1	110	2	S36258	Ig lambda chain V
32	41	66.1	112	2	LIHUM	Ig lambda chain V
33	41	66.1	130	2	S09712	Ig lambda chain V
34	41	66.1	186	2	F86379	Ig lambda chain V
35	41	66.1	393	2	H75444	protein F21J9.28 (
36	41	66.1	429	2	AC2248	branchcd-chain ami
37	39	62.9	130	1	LIHUB	enolase (imported)
38	39	62.9	324	2	S62543	Ig lambda chain pr
39	39	62.9	430	2	S28707	hypothetical prote
40	39	62.9	719	2	S61046	hypothetical prote
41	38	61.3	107	2	B46516	ARPI protein - yea
42	38	61.3	131	2	S24321	Ig lambda chain V
43	38	61.3	217	2	JF0246	Ig lambda chain pr
44	38	61.3	347	2	S64936	Ig lambda chain NI
45	38	61.3	398	2	F84957	probable membrane
						1-deoxy-D-xyulose

ALIGNMENTS

RESULT 1
S36046
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S36046
R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36046
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <WILD>
A:Cross-references: EMBL:Z22187; NID:q312312; PIDN:CA80197.1; PID:q312313
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 88.7%; Score 55; DB 2; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.01;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSSSNIGINAVN 13
DB 23 SGSSSNIGINAVN 35

RESULT 2

A44151
Ig lambda chain V region (BO-08) - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

R:Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Goethien, R.H.; Graff, R.; DeGraw, J.;
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992

A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746

A:Accession: A44151
A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-112 <ZEB>

A>Note: nucleotide translation not given
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F,14-90/Domain; immunoglobulin homology <IMM>

Query Match 85.5%; Score 53; DB 2; Length 112;
Best Local Similarity 84.6%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SGSSSNIGINAVN 13

Db 22 SGSSSNTGNTVN 34

RESULT 3

Ig lambda chain V region (BO-09) - human (fragment)
B44151
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: B44151
R:Zebdege, S.L.; Barbas III, C.F.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.; Pye
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746
A:Accession: B44151
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-112 <ZEB>
A:Cross-references: GB:M88310; NID:9183954; PIDN:AAA35968.1; PID:9183955
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 53; DB 2; Length 112;
Best Local Similarity 84.6%; Pred. No. 0.026; 2; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 SGSSSNTGNTVN 13
Db 22 SGSSSNTGNTVN 34

RESULT 4

Ig lambda chain - human (fragment)
S36047
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36047
R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36047
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <WIL>
A:Cross-references: EMBL:222188; NID:9312291; PIDN:CAA80198.1; PID:9312292
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 52; DB 2; Length 98;
Best Local Similarity 84.6%; Pred. No. 0.035; 2; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 SGSSSNTGNTVN 13
Db 23 SGSSSNTGNTVN 35

RESULT 5

Ig lambda chain V region (BO-12) - human (fragment)
D44151
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: D44151
R:Zebdege, S.L.; Barbas III, C.F.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.; Pye
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746
A:Accession: D44151
A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
A:Residues: 1-112 <ZEB>
A>Note: nucleotide translation is not given
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 52; DB 2; Length 112;
Best Local Similarity 84.6%; Pred. No. 0.04; 2; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 SGSSSNTGNTVN 13
Db 22 SGSSSNTGNTVN 34

RESULT 6

Ig lambda chain precursor - human
S23627
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S23627
R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Delfos, M.; Kozin, F.; Carson, D.A.
J. Exp. Med. 175, 831-842, 1992
A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro
A:Reference number: S23623; MUID:92156804
A:Accession: S23627
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <OLE>
A:Cross-references: EMBL:X59707; NID:934426; PIDN:CAA2228.1; PID:934427
C:Genetics:
A:Introns: 16/1
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 52; DB 2; Length 117;
Best Local Similarity 84.6%; Pred. No. 0.042; 2; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 SGSSSNTGNTVN 13
Db 42 SGSSSNTGNTVN 54

RESULT 7

Ig lambda chain - human
S25752
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25752
R:Combrato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin
A:Reference number: S16439; MUID:91257162
A:Accession: S25752
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57817; NID:933733; PIDN:CAA40954.1; PID:933734
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:146-216/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 52; DB 2; Length 233;
Best Local Similarity 84.6%; Pred. No. 0.086; 2; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 SGSSSNTGNTVN 13

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:48:18 ; Search time 52.75 Seconds

(without alignments)
9.542 Million cell updates/sec

Title: US-09-780-035-29_COPY_23_35

Sequence: 1 SGSSSNGICNAVN 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	71.0	109	LV11_HUMAN	P06888 homo sapien
2	44	71.0	111	LV1D_HUMAN	P01702 homo sapien
3	41	66.1	112	LV1H_HUMAN	P06887 homo sapien
4	39	62.9	130	LV1G_HUMAN	P06316 homo sapien
5	39	62.9	324	YAGC_SCHPO	Q09875 schizosacch
6	39	62.9	430	MAS1_AGRU	P50202 agrobacteri
7	39	62.9	719	NRPI_YEAST	P32770 saccharomyc
8	38	61.3	398	DKR_BUCAL	P57329 buchenera ap
9	37	59.7	111	LV1C_HUMAN	P01701 homo sapien
10	37	59.7	374	PE1L_ERMCA	P11430 erwinia car
11	37	59.7	375	PE1L_ERMCA	P04959 erwinia chr
12	37	59.7	528	ASM4_YEAST	Q05166 saccharomyc
13	36	58.1	356	DKR_CAMUTE	Q09mv3 campylobact
14	36	58.1	374	PE1L_ERMCA	P11431 erwinia car
15	36	58.1	379	CYB_LDMTE	Q34945 lumbricus t
16	36	58.1	381	CYB_ARTSF	Q37713 artemia san
17	36	58.1	397	POR_CHURE	Q39617 chlamydomon
18	36	58.1	433	HEM2_SPIOT	P24493 spinaclia cl
19	36	58.1	462	NHAC_BACRI	P27611 bacillus fi
20	36	58.1	513	GNTR_BACIT	P46834 bacillus ii
21	36	58.1	513	GNTR_BACIT	P46834 bacillus ii
22	36	58.1	513	GNTR_BACIT	P46834 bacillus ii
23	35	56.5	103	LV1E_HUMAN	P51862 saccharomyc
24	35	56.5	220	YS18_BORBU	P01703 homo sapien
25	35	56.5	426	YMW8_YEAST	P70842 borrelia bu
26	35	56.5	438	ENO_ASPOK	Q04749 saccharomyc
27	35	56.5	686	FMA_ARATH	Q13560 aspergillus
28	35	56.5	1329	FTSK_ECOCI	Q91v16 arabidopsis
29	34.5	55.6	194	IPCA_HAEPU	P46889 escherichia
30	34.5	55.6	1022	CA26_CHICK	O87340 haemophilus
31	34	54.8	109	LV1E_HUMAN	P15988 gallus gall
32	34	54.8	111	LV1A_HUMAN	P04208 homo sapien
33	34	54.8	216	HPD1_HAEIN	P01699 homo sapien
					P45992 haemophilus

34	54.8	272	1	RSRL_YEAST	P13856 saccharomyc
35	54.8	328	1	ZIPA_HAEIN	P44113 haemophilus
36	54.8	416	1	FTSY_NEIGO	P14929 neisseria g
37	54.8	421	1	FTSY_NEIMA	P57010 neisseria m
38	54.8	421	1	FTSY_NEIMB	P57011 neisseria m
39	54.8	421	1	FTSY_NEIMC	O30391 neisseria m
40	54.8	426	1	SYH_THEAC	O9h1x5 thermoplasm
41	54.8	458	1	FMCL_PSEAE	O51404 pseudomonas
42	54.8	464	1	FMCL_PSEAE	P71384 haemophilus
43	54.8	509	1	FLAA_HELPY	Q03843 helicobacte
44	54.8	517	1	ME1A_SCHPO	O13606 schizosacch
45	54.8	543	1	MIG1_KIDUA	P52288 kluyveromyc

ALIGNMENTS

RESULT 1	
LV11_HUMAN	
ID	LV11_HUMAN
AC	P06888;
DT	01-JAN-1988 (Rel. 06, Created)
DT	01-JAN-1988 (Rel. 06, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig lambda chain V-I region EPS.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=86000126; PubMed=3929803;
RA	Toft K.G., Sletten K., Husby G.;
RT	"The amino-acid sequence of the variable region of a carbohydrate-
RT	containing amyloid fibril protein EPS (immunoglobulin light chain,
RT	type lambda).";
RL	Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC	-I- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
CC	PEPTIDES WERE POSITIONED BY HOMOLOG.
DR	PIR; A24656; LIHUP.
DR	HSSP; P01703; 7FAB.
DR	InterPro; IPR003006; IG_MHC.
DR	InterPro; IPR003596; IG_V.
DR	Pfam; PF00047; Ig; 1.
KW	SMART; SM00406; IgV; 1.
FT	Immunoglobulin V region; Amyloid; Glycoprotein.
FT	CARBOHYD 104 104
FT	DISULFD 22 89
FT	NON_TER 109 109
FT	SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;
QY	1 SGSSSNGICNAVN 13
DB	23 SGSSSNGICKNYVD 35
QY	1 SGSSSNGICNAVN 13
DB	23 SGSSSNGICKNYVD 35
RESULT 2	
LV1D_HUMAN	
ID	LV1D_HUMAN
AC	P01702;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig lambda chain V-I region NIG-64.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;

Query Match 71.0%; Score 44; DB 1; Length 109;
Best Local Similarity 76.9%; Pred. No. 0.41;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

RN [1]
RP SEQUENCE.
RX MEDLINE-83186114; PubMed-6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup."
RL J. Biochem. 93:421-429(1983).
DR PIR: A01965; LIHUNG.
DR HSSP: P01703; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1
FT DISULFID 22
FT NON_TER 111
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

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Query Match 71.0%; Score 44; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.41;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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OY 1 SGSSSNIGINAVN 13
DB 23 SGSSSNIGNDYVS 35

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RESULT 3
LV1H_HUMAN STANDARD; PRT; 112 AA.
ID LV1H_HUMAN
AC P06887;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE-85257662; PubMed-2410269;
RA Mibessco E., Roy J.P., Congy N., Peran-Rivat L., Mibessco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features."
RL Eur. J. Biochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
CC WERE POSITIONED BY HOMOLOG.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
CC MARKERS.
DR PIR: A25479; LIHUM.
DR HSSP: P01703; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT MOD_RES 1
FT DISULFID 22
FT NON_TER 112
SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFBE4 CRC64;

```

```

Query Match 66.1%; Score 41; DB 1; Length 112;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

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OY 1 SGSSSNIGIN 10
DB 23 SGSSSNVGSN 32

```

```

RESULT 4
LV1G_HUMAN STANDARD; PRT; 130 AA.
ID LV1G_HUMAN
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-85062823; PubMed-6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
RT sequence."
RL Nucleic Acids Res. 12:8407-8414(1984).

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CC use by non-profit institutions as long as its content is in no way
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DR EMBL: X01147; CAA25598.1; -.
DR PIR: A01966; LIHUBL.
DR HSSP: P01703; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT DISULFID 41 108 BY SIMILARITY.
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 13564 MW; FA44BB17D3A55EBF CRC64;

```

```

Query Match 62.9%; Score 39; DB 1; Length 130;
Best Local Similarity 69.2%; Pred. No. 3.8;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1 SGSSSNIGINAVN 13
DB 42 SGSSSNIGNDYVS 54

```

```

RESULT 5
YAGC_SCHPO STANDARD; PRT; 324 AA.
ID YAGC_SCHPO
AC O09875;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Hypothetical 35.8 kDa protein C12G12.12 in chromosome I.
GN SPAC12G12.12.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;

```


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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:22 ; Search time 194.32 Seconds

(without alignments)
11.573 Million cell updates/sec

Title: us-09-780-035-29_COPY_23_35

Perfect score: 62

Sequence: 1 SSSSSNIGINAV 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 segs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	71.0	108	4	Q96SB0
2	43	69.4	769	16	Q92KK3
3	42	67.7	146	10	Q9FJX2
4	41	66.1	186	10	Q9FYK2
5	41	66.1	393	16	Q9RVU0
6	39	62.9	567	5	Q9V925
7	39	62.9	607	5	Q960E4
8	38	61.3	158	5	Q9GRY0
9	38	61.3	184	5	Q9VBAB
10	38	61.3	193	17	Q9H1F8
11	38	61.3	199	11	Q921F8
12	38	61.3	347	3	Q12452
13	38	61.3	414	11	Q9D6K9
14	38	61.3	414	11	Q924K3
15	38	61.3	447	10	Q9SU41
16	38	61.3	454	5	Q9GV74

17	38	61.3	476	10	Q9SWE2
18	38	61.3	476	10	Q940M2
19	38	61.3	488	5	Q96693
20	38	61.3	608	16	Q977Y3
21	38	61.3	1056	5	Q9BHJ4
22	38	61.3	1935	5	Q9VOM0
23	37	59.7	86	11	Q9JIV2
24	37	59.7	353	2	Q04086
25	37	59.7	331	2	Q93423
26	37	59.7	391	2	Q93414
27	37	59.7	395	16	Q97K07
28	37	59.7	401	5	Q9X7Y4
29	37	59.7	435	5	Q9P452
30	37	59.7	444	2	Q93A22
31	37	59.7	488	5	Q76962
32	37	59.7	519	16	Q9CDN5
33	37	59.7	528	5	Q9VUM4
34	37	59.7	534	5	Q9NKR6
35	37	59.7	549	5	Q9BK85
36	37	59.7	593	5	Q9X7Y6
37	37	59.7	601	3	Q9C1I3
38	37	59.7	632	5	Q9VHC7
39	37	59.7	805	5	Q22143
40	37	59.7	1048	2	Q9LA04
41	37	59.7	1048	2	Q48804
42	37	59.7	1472	5	Q9V358
43	37	59.7	3930	16	Q9BE20
44	37	59.7	4845	11	Q88738
45	36.5	58.9	343	12	Q91C66

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	108 AA.
Q96SB0			
AC	Q96SB0;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)		
DE	ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN		
DE	VARIABLE REGION (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98375893; PubMed=9712075;		
RA	Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;		
RT	"Molecular analysis of polyclonal monoclonal antibodies from		
RT	rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin		
RT	antibody V region genes."		
RT	J. Immunol. 161:2020-2031(1998).		
DR	EMBL; U96394; AAB68783.1; ..		
FT	NON_TER		
FT	SEQUENCE	108 AA;	11594 MW; F4B5DC478A043F48 CRC64;

Query Match 71.0%; Score 44; DB 4; Length 108;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SSSSSNIGINAV 12
DB 23 SSSSSNIGSNV 34

RESULT 2
ID Q92KK3 PRELIMINARY: PRT: 769 AA.
AC Q92KK3;

Query Match	Similarity	69.4%	Score 43	DB 16	Length 769
Best Local	Similarity	81.8%	Pred. No. 43		
Matches	9	Conservative	1	Mismatches	1
				Indels	0
				Gaps	0
QY	1	SGSSGNIGINA	11		
		:			
Db	746	SGSSGNIGISA	756		

Query Match	67.7%;	Score 42;	DB 10;	Length 146;
Best Local Similarity	53.8%;	Pred. No. 10;		

[illegible]

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:18 ; Search time 245.49 Seconds

(without alignments)
3.167 Million cell updates/sec

Title: us-09-780-035-29_COPY_51_57

Perfect score: 39

Sequence: 1 GNDGRPS 7

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	39	100.0	7	21	AA1981.DAT:*
3	39	100.0	7	21	AA1982.DAT:*
4	39	100.0	7	21	AA1983.DAT:*
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8	39	100.0	7	21	AA1987.DAT:*
9	39	100.0	7	21	AA1988.DAT:*
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11	39	100.0	7	21	AA1990.DAT:*
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23	39	100.0	112	21	AA1991.DAT:*
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27	39	100.0	112	21	AA1995.DAT:*
28	39	100.0	112	21	AA1996.DAT:*
29	39	100.0	112	21	AA1997.DAT:*
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31	39	100.0	112	21	AA1999.DAT:*
32	39	100.0	112	21	AA2000.DAT:*
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37	39	100.0	112	21	AA2005.DAT:*
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ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description
1	AA1980.DAT:*	39	100.0	7	21	AA1980.DAT:*
2	AA1981.DAT:*	39	100.0	7	21	AA1981.DAT:*
3	AA1982.DAT:*	39	100.0	7	21	AA1982.DAT:*
4	AA1983.DAT:*	39	100.0	7	21	AA1983.DAT:*
5	AA1984.DAT:*	39	100.0	7	21	AA1984.DAT:*
6	AA1985.DAT:*	39	100.0	7	21	AA1985.DAT:*
7	AA1986.DAT:*	39	100.0	7	21	AA1986.DAT:*
8	AA1987.DAT:*	39	100.0	7	21	AA1987.DAT:*
9	AA1988.DAT:*	39	100.0	7	21	AA1988.DAT:*
10	AA1989.DAT:*	39	100.0	7	21	AA1989.DAT:*
11	AA1990.DAT:*	39	100.0	7	21	AA1990.DAT:*
12	AA1991.DAT:*	39	100.0	7	21	AA1991.DAT:*
13	AA1992.DAT:*	39	100.0	7	21	AA1992.DAT:*
14	AA1993.DAT:*	39	100.0	7	21	AA1993.DAT:*
15	AA1994.DAT:*	39	100.0	7	21	AA1994.DAT:*
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18	AA1997.DAT:*	39	100.0	7	21	AA1997.DAT:*
19	AA1998.DAT:*	39	100.0	7	21	AA1998.DAT:*
20	AA1999.DAT:*	39	100.0	7	21	AA1999.DAT:*
21	AA2000.DAT:*	39	100.0	7	21	AA2000.DAT:*
22	AA2001.DAT:*	39	100.0	7	21	AA2001.DAT:*

DR WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to

PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's

PT disease and multiple sclerosis -

XX

XX Claim 24; Page 232; 377pp; English.

XX

CC This invention relates to a new human antibody specific for human

CC interleukin-12 (IL-12). The invention also includes antigen binding

CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human

CC anti-IL-12 antibody heavy and light chain complementarity determining

CC region (CDR) amino acid sequences, and also includes variable region

CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771

CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063

CC represent other CDR sequences. Light chain CDR3 consensus sequences are

CC given in AAB40064-B40067. Primers used in the identification and

CC construction of the antibodies of the invention are given in

CC AAB61062-C61071. The antibody of the invention is a neutralizing

CC antibody and has antirheumatic; antiarthritic; antisclerotic;

CC antiinflammatory; neuroprotective; antipsoriatic; antistomatitic;

CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.

CC The antibodies or antigen-binding fragments are useful in the treatment

CC of disorders associated with detrimental release of human IL-12,

CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.

CC They can also be used in the manufacture of a pharmaceutical composition

CC to treat human IL-12 disorders.

XX

SQ Sequence 7 AA;

XX

Query Match 100.0%; Score 39; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNDORPS 7

Db 1 gndqrps 7

|||||

RESULT 2

AAB40001

ID AAB40001 standard; Peptide; 7 AA.

XX

AC AAB40001;

XX

DT 05-FEB-2001 (first entry)

XX

DE Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 517.

XX

DE Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;

KW complementarity determining region; CDR; antirheumatic; antiarthritic;

KW antisclerotic; neuroprotective; antipsoriatic; antistomatitic; cardiant;

KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;

KW multiple sclerosis; rheumatoid arthritis.

XX

OS Homo sapiens.

XX

PN WO200056772-A1.

XX

PD 28-SEP-2000.

XX

PF 24-MAR-2000; 2000WO-US07946.

XX

PR 25-MAR-1999; 99US-0126603.

XX

XX (BADI) BASF AG.

PA (GEMY) GENETICS INST INC.

XX

PI Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;

PI Kaymacalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;

PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;

PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX

XX New human antibody specific for human interleukin-12 (IL-12) used to

PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's

PT disease and multiple sclerosis -

XX

XX Claim 33; Figure 2G; 377pp; English.

XX

CC This invention relates to a new human antibody specific for human

CC interleukin-12 (IL-12). The invention also includes antigen binding

CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human

CC anti-IL-12 antibody heavy and light chain complementarity determining

CC region (CDR) amino acid sequences, and also includes variable region

CC amino acid sequences. Other variable region amino acid sequences are

CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771

CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063

CC represent other CDR sequences. Light chain CDR3 consensus sequences are

CC given in AAB40064-B40067. Primers used in the identification and

CC construction of the antibodies of the invention are given in

CC AAB61062-C61071. The antibody of the invention is a neutralizing

CC antibody and has antirheumatic; antiarthritic; antisclerotic;

CC antiinflammatory; neuroprotective; antipsoriatic; antistomatitic;

CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.

CC The antibodies or antigen-binding fragments are useful in the treatment

CC of disorders associated with detrimental release of human IL-12,

CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.

CC They can also be used in the manufacture of a pharmaceutical composition

CC to treat human IL-12 disorders.

XX

SQ Sequence 7 AA;

XX

Query Match 100.0%; Score 39; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNDORPS 7

Db 1 gndqrps 7

|||||

RESULT 3

AAB40013

ID AAB40013 standard; Peptide; 7 AA.

XX

AC AAB40013;

XX

DT 05-FEB-2001 (first entry)

XX

DE Anti-hIL12 antibody light chain CDR2 amino acid sequence SEQ ID 529.

XX

DE Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;

KW complementarity determining region; CDR; antirheumatic; antiarthritic;

KW antisclerotic; neuroprotective; antipsoriatic; antistomatitic; cardiant;

KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;

KW multiple sclerosis; rheumatoid arthritis.

XX

OS Homo sapiens.

XX

PN WO200056772-A1.

XX

PD 28-SEP-2000.

XX

PF 24-MAR-2000; 2000WO-US07946.

XX

PR 25-MAR-1999; 99US-0126603.

XX

XX (BADI) BASF AG.

PA (GEMY) GENETICS INST INC.

XX

PI Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;

Pt	* Kaymakcalan Z., Labkovsky B., Sakoraitch S., Friedrich S., Myles A.; Pi Velman GM, Venturini A., Wayne NW, Widom A, Edwin JG, Duncan AR; PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL, XX WPI, 2000-638250/61.
DR XX	New human antibody specific for human interleukin-12 (IL-12) used to PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's PR disease and multiple sclerosis -
XN PS	Clalm 33; Figure 2g; 377pp; English.
CC CC	This invention relates to a new human antibody specific for human interleukin-12 (IL-12). The invention also includes antigen binding portions that bind to IL-12. Sequences AAB39485-B39516 represent human anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences, and also includes variable region amino acid sequences. Other variable region amino acid sequences are given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771 represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063 represent other CDR sequences. Light chain CDR3 consensus sequences are given in AAB40064-B40067. Primers used in the identification and construction of the antibodies of the invention are given in AAG61052-661071. The antibody of the invention is a neutralising antibody and has antirheumatic; antiarthritic; antisclerotic; anti-inflammatory; neuroprotective; antidepressant; antispasmodic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. The antibodies or antigen-binding fragments are useful in the treatment of disorders associated with detrimental release of human IL-12, especially Crohn's disease, multiple sclerosis and rheumatoid arthritis. They can also be used in the manufacture of a pharmaceutical composition to treat human IL-12 disorders.
SQ XX	Sequence 7 AA:
OY Db	Query Match Best Local Similarity 100.0%; Score 39; DB 21; Length 7; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dy	1 GNDQRPS 7 Db 1 gndqrs 7
RESULT 4	
ID AAY79089	AAY79089 standard; peptide; 7 AA.
AC XX	AAY79089;
DT DT	12-JUN-2000 (first entry)
DE XX	Anti-factor IX/Xa antibody L chain V domain CDR2 amino acid sequence.
KW KW	Complementarily determining region 2, CDR2; antibody; Gla domain; factor IX/Xa; blood coagulation; deep venous thrombosis; light chain; arterial thrombosis; unstable angina; post myocardial infarction; coronary artery bypass graft; CABG; stroke; tumour growth; metastasis; percutaneous transluminal coronary angioplasty; PCA; inflammation; septic shock; hypotension; adult respiratory distress syndrome; ARDS; arterial fibrillation; disseminated intravascular coagulopathy; DIC.
OS XX	Homo sapiens.
PN PN	WO200012562-A1.
PD PD	09-MAR-2000.
PF PF	26-AUG-1999; 99WO-US19453.
RK RK	28-AUG-1998; 98US-0098233. 03-MAR-1999; 99US-0122767.

[illegible]

PI Chayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI Duncan AR, Brocchietti SM, Mankovich J, Shorrock CP, Thompson JE

DR WPI; 2001-550020/61.
DR N-PSDB; AAH47514.

XX: Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX
 PS Example 2; Page 90; 91pp; English.
 CC
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LT28
 CC light chain sequence.
 CC
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 39; DB 22; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.91;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNDQRRS 7
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 DB 51 gndqrps 57

RESULT 8
 AAB39508
 ID AAB39508 standard; Protein; 112 AA.
 XX
 AC AAB39508;
 XX
 DT 05-FEB-2001 (first entry)
 DE
 DE Anti-IL-12 antibody L chain variable region amino acid sequence #24.
 XX
 KW Human: neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR: antirheumatic; antiarthritis;
 KW antisclerotic; neuroprotective; antipsoriatic; antilastmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN MO200056772-A1.
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000MO-US07946.
 XX
 PR 25-MAR-1999; 99US-0126603.
 XX
 PA (BADI) BASF AG.
 PA (GENY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
 XX
 WPI; 2000-638250/61.

PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX
 PS Claim 26; Page 141; 377pp; English.
 CC
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-839516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-839560 and AAB40068-840149. Sequences AAB39561-839771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-840063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-840067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAC61062-661071. The antibody of the invention is a neutralising
 CC antibody and has antirheumatic; antiarthritis; antisclerotic;
 CC antiinflammatory; neuroprotective; antipsoriatic; antilastmatic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 CC
 XX
 SQ Sequence 112 AA;

Query Match 100.0%; Score 39; DB 21; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNDQRRS 7
 |||||
 DB 51 gndqrps 57

RESULT 9
 AAB39518
 ID AAB39518 standard; Protein; 112 AA.
 XX
 AC AAB39518;
 XX
 DT 05-FEB-2001 (first entry)
 DE
 DE Anti-IL12 antibody V chain variable region amino acid sequence SEQ ID 34.
 XX
 KW Human: neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR: antirheumatic; antiarthritis;
 KW antisclerotic; neuroprotective; antipsoriatic; antilastmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN MO200056772-A1.
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000MO-US07946.
 XX
 PR 25-MAR-1999; 99US-0126603.
 XX
 PA (BADI) BASF AG.
 PA (GENY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
 XX
 WPI; 2000-638250/61.

DR WPI: 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX
 PS Example 1; Figure 1; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAB61062-C61071. The antibody of the invention is a neutralizing
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antiparasitic; antiparasitic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 CC
 SQ Sequence 112 AA;
 XX
 XX

Query Match 100.0%; Score 39; DB 21; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNDORPS 7
 |||||
 Db 51 gndqrps 57

RESULT 10
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 ID AAB39522 standard; Protein; 112 AA.
 XX
 AC AAB39522;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody V chain variable region amino acid sequence SEQ ID 38.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparasitic; antiparasitic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US07946.
 XX
 PR 25-MAR-1999; 99US-0126603.
 XX
 PA (BADI) BASF AG.
 PA (GEMV) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;

PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
 XX
 DR WPI: 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis -
 XX
 PS Example 1; Figure 1; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Primers used in the identification and
 CC construction of the antibodies of the invention are given in
 CC AAB61062-C61071. The antibody of the invention is a neutralizing
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;
 CC antiinflammatory; neuroprotective; antiparasitic; antiparasitic;
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
 CC The antibodies or antigen-binding fragments are useful in the treatment
 CC of disorders associated with detrimental release of human IL-12,
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 CC
 SQ Sequence 112 AA;
 XX
 XX

Query Match 100.0%; Score 39; DB 21; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNDORPS 7
 |||||
 Db 51 gndqrps 57

RESULT 11
 AAB39524
 ID AAB39524 standard; Protein; 112 AA.
 XX
 AC AAB39524;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody V chain variable region amino acid sequence SEQ ID 40.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparasitic; antiparasitic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US07946.
 XX
 PR 25-MAR-1999; 99US-0126603.
 XX
 PA (BADI) BASF AG.
 PA (GEMV) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;

PI Kaymakçalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR,
PI Derbyshire EJ, Carmen S, Smith S, Hollett TL, Du Fou SL,
XX WPI: 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis -
XX

PS Example 1; Figure 1; 377pp; English.

XX This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
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CC given in AAB39517-B39560 and AAB40066-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibody of the invention are given in
CC AAC61062-C61071. The antibody of the invention is a neutralising
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CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.
CC The antibodies or antigen-binding fragments are useful in the treatment
CC of disorders associated with detrimental release of human IL-12,
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX

SO Sequence 112 AA:

Query Match 100.0%; Score 39; DB 21; Length 112;

Best Local Similarity 100.0%; Pred. No. 0.92; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNDORPS 7
| | | | | | |

DB 51 gndqrrps 57

RESULT 12

AAB39526 standard; Protein; 112 AA.

AC AAB39526;

DT 05-FEB-2001 (first entry)

DE Anti-IL12 antibody V chain variable region amino acid sequence SEQ ID 42.

XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritis;
XX antileukemic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

PN WO200056772-A1.

PD 28-SEP-2000.

PE 24-MAR-2000; 2000WO-US07946.

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PA (GEMY) GENETICS INST INC.
XX

XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
PI Kaymakçalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR,
PI Derbyshire EJ, Carmen S, Smith S, Hollett TL, Du Fou SL,
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CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.
XX

SO Sequence 112 AA:

Query Match 100.0%; Score 39; DB 21; Length 112;

Best Local Similarity 100.0%; Pred. No. 0.92; 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNDORPS 7
| | | | | | |

DB 51 gndqrrps 57

RESULT 13

AAB39528 standard; Protein; 112 AA.

AC AAB39528;

DT 05-FEB-2001 (first entry)

DE Anti-IL12 antibody V chain variable region amino acid sequence SEQ ID 44.

XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
XX complementarity determining region; CDR; antirheumatic; antiarthritis;
XX antileukemic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;
XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
XX multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

PN WO200056772-A1.

PD 28-SEP-2000.

PE 24-MAR-2000; 2000WO-US07946.

PF 25-MAR-1999; 99US-0126603.
PR
XX

PA (BADI) BASF AG.
 PA (GEMV) GENETICS INST INC.
 XX
 PI Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
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 XX WPI: 2000-638250/61.
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 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.
 CC They can also be used in the manufacture of a pharmaceutical composition
 CC to treat human IL-12 disorders.
 CC
 CC Sequence 112 AA;
 XX
 SQ
 Query Match 100.0%; Score 39; DB 21; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GNDORPS 7
 |||||
 Db 51 gndqprs 57
 RESULT 14
 AAB39530
 ID AAB39530 standard; Protein; 112 AA.
 AC AAB39530;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody V chain variable region amino acid sequence SEQ ID 46.
 XX
 KW Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparasitic; antisthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US07946.
 XX

PR 25-MAR-1999; 99US-0126603.
 XX
 PA (BADI) BASF AG.
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 PI Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elyin JG, Duncan AR;
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 XX WPI: 2000-638250/61.
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 CC
 CC Sequence 112 AA;
 XX
 SQ
 Query Match 100.0%; Score 39; DB 21; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GNDORPS 7
 |||||
 Db 51 gndqprs 57
 RESULT 15
 AAB39532
 ID AAB39532 standard; Protein; 112 AA.
 AC AAB39532;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody V chain variable region amino acid sequence SEQ ID 48.
 XX
 KW Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparasitic; antisthmatic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX

PF 24-MAR-2000: 2000MO-US07946.

XX 25-MAR-1999: 99US-0126603.

PA (BADI) BASF AG.
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PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakçalan Z, Iakovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GW, Venturini A, Warner NW, Widom A, Elvin JG, Duncan AR;
PI Deryshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;
DR WPI: 2000-638250/61.

PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
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PS Example 1: Figure 1: 377pp: English.

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CC They can also be used in the manufacture of a pharmaceutical composition
CC to treat human IL-12 disorders.

Sequence 112 AA;

Query Match 100.0%; Score 39; DB 21; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNDORPS 7
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Db 51 gndqtps 57

Search completed: June 21, 2002, 09:20:18
Job time: 431 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:43 ; Search time 109.39 Seconds

(without alignments)
6.149 Million cell updates/sec

Title: US-09-780-035-29_COPY_51_57

Perfect score: 39

Sequence: 1 GNDORPS 7

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.71:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	89.7	198	2	C32998
2	33	84.6	395	2	T51021
3	33	84.6	447	2	A64934
4	33	84.6	447	2	C90935
5	33	84.6	447	2	G85783
6	33	84.6	1087	2	T30330
7	33	84.6	1213	2	A41724
8	32	82.1	245	1	RDEBIV
9	32	82.1	341	2	B86633
10	32	82.1	347	2	T48610
11	32	82.1	875	2	S62177
12	31	79.5	101	2	AH1914
13	31	79.5	238	2	AC2573
14	31	79.5	326	2	A83273
15	31	79.5	402	2	A84766
16	31	79.5	412	2	F89905
17	31	79.5	533	2	B26446
18	31	79.5	1148	2	F69685
19	30	76.9	109	2	T17831
20	30	76.9	171	2	D84302
21	30	76.9	234	1	F65080
22	30	76.9	234	2	C91107
23	30	76.9	234	2	F85952
24	30	76.9	269	2	E72693
25	30	76.9	316	2	G84187
26	30	76.9	323	2	T00244
27	30	76.9	342	2	T13113
28	30	76.9	465	2	E75474
29	30	76.9	483	2	E83359

30	30	76.9	509	2	JC6203	SPB binding protei
31	30	76.9	570	2	E95978	hypothetical prote
32	30	76.9	593	2	A64775	ABC-type transport
33	30	76.9	593	2	G90691	ABC-type transport
34	30	76.9	593	2	G85542	ABC-type transport
35	30	76.9	614	2	F89793	conserved hypothet
36	30	76.9	615	2	A83188	hypothetical prote
37	30	76.9	616	2	E83485	probable lonb-depe
38	30	76.9	908	2	AE2254	hypothetical mal f
39	30	76.9	1143	4	I84547	hypothetical mal f
40	30	76.9	1388	2	T30335	KLP2 protein - Afr
41	30	76.9	1679	2	S48385	hypothetical prote
42	30	76.9	1796	2	AC1895	serine/threonine k
43	30	76.9	1941	2	T30554	ubiquitin-protein
44	29	74.4	941	2	S72626	small-cell-variant
45	29	74.4	113	2	A29700	Ig lambda chain V

ALIGNMENTS

RESULT 1
C32998
Chorion protein S19 - fruit fly (Drosophila virilis)
C:Species: Drosophila virilis
C:Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change 24-Sep-1998
C:Accession: C32998
R.Fenerjlan, M.G.; Martinez-Cruzado, J.C.; Swimmer, C.; King, D.; Kafatos, F.C.
J. Mol. Evol. 29, 108-125, 1989
A:Title: Evolution of the autosomal chorion cluster in Drosophila. II. Chorion gene e
A:Reference number: A32998; MUID:90040741
A:Accession: C32998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-198 <FEN>
A:Cross-References: GB:X53421; NID:g9164; PID:g9167; GB:X12636; GB:X16717
C:Genetics:
A:Gene: FlyBase:IDVlr/Cp19
A:Cross-References: FlyBase:FBgn0013071

Query Match 89.7%; Score 35; DB 2; Length 198;
Best Local Similarity 100.0%; Pred.No. 3.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNDORP 6
|||||
Db 59 GNDORP 64

RESULT 2
T51021
related to hydroxymethylglutaryl-CoA lyase [imported] - Neurospora crassa
N:Alternate names: protein B7F21.20
C:Species: Neurospora crassa
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
R.Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, July 2000
A:Reference number: 225286
A:Accession: T51021
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SCH>
A:Cross-References: EMBL:AL389901; GSPDB:GN00116; NCSP:B7F21.20
A:Experimental source: BAC clone B7F21; strain OR74A
C:Genetics:
A:Gene: NCSP:B7F21.20
A:Map position: 6
A:Introns: 107/3

Query Match 84.6%; Score 33; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NDORPS 7
|||||
Db 40 NDORPS 45

RESULT 3

A64934

Succinylarginine dihydrolase (EC 3.-.-.-) - Escherichia coli (strain K-12)

C/Species: Escherichia coli

C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 31-Dec-2001

C/Accession: A64934

R/Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Ch.

A: Rose, D.J.; Mau, B.; Shao, Y.

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617

A/Accession: A64934

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-447 <BLAST>

A/Cross-references: GB:A6000269; GB:U00096; NID:q1788033; PIDN:AACT4815.1; PID:q1788041;

A/Experimental source: strain K-12, substrain MG1655

C/Superfamily: Escherichia coli hypothetical protein b1745

C/Keywords: hydrolase

Query Match 84.6%; Score 33; DB 2; Length 447;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNDORPS 7
|||||
Db 201 GNDORPS 207

RESULT 4

C90935

hypothetical protein ECS2451 [imported] - Escherichia coli (strain O157:H7, substrain R1

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C/Accession: C90935

R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene

A/Reference number: A93629; MUID:21156231; PMID:11258796

A/Accession: C90935

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-447 <HAY>

A/Cross-references: GB:BA000007; PIDN:BA035874.1; PID:q13361918; GSPDB:GN00154

A/Experimental source: strain O157:H7, substrain R1MD 0509952

C/Genetics:

A/Gene: ECS2451

C/Superfamily: Escherichia coli hypothetical protein b1745

Query Match 84.6%; Score 33; DB 2; Length 447;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNDORPS 7
|||||
Db 201 GNDORPS 207

RESULT 5

G85783

hypothetical protein Z2777 [imported] - Escherichia coli (strain O157:H7, substrain EDL9

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C/Accession: G85783

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dialante, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: G85783

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-447 <STO>

A/Cross-references: GB:A6005174; NID:q12515764; PIDN:AAG56731.1; GSPDB:GN00145; UMGF:

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: Z2777

C/Superfamily: Escherichia coli hypothetical protein b1745

Query Match 84.6%; Score 33; DB 2; Length 447;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNDORPS 7
|||||
Db 201 GNDORPS 207

RESULT 6

T30330

gelsolin-related protein GRP125 - slime mold (Dictyostellium discoideum)

C/Species: Dictyostellium discoideum

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C/Accession: T30330

R/Stocker, S.; Hiery, M.; Marriot, G.

Mol. Biol. Cell 10, 161-178, 1999

A/Title: Phototactic migration of Dictyostellium cells is linked to a new type of gels

A/Reference number: Z20823; MUID:99096692

A/Accession: T30330

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1087 <STO>

A/Cross-references: EMBL:U95159; NID:q4100185; PID:q4100186; PIDN:AAD00774.1

C/Genetics:

A/Introns: 137/1

Query Match 84.6%; Score 33; DB 2; Length 1087;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NDORPS 7
|||||
Db 670 NDORPS 675

RESULT 7

A41724

limb deformity (ld) protein - chicken

C/Species: Gallus gallus (chicken)

C/Date: 04-Mar-1993 #sequence_revision 15-Aug-1997 #text_change 10-Sep-1997

C/Accession: S24286; S38780; A41724

R/Timp, A.; Blundell, P.A.; de la Pompa, J.L.; Zeller, R.

Genes Dev. 6, 14-28, 1992

A/Title: The chicken limb deformity gene encodes nuclear proteins expressed in specifi

A/Reference number: A41724; MUID:92112031

A/Accession: S24286

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-1213 <TRU>

A/Cross-references: EMBL:X62681

A/Experimental source: embryo

R/Zeller, R.

submitted to the EMBL Data Library, August 1991


```

OS  Vibrio alginolyticus.
OC  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX  NCBI_TaxID=663;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=138-2;
RA  MEDLINE=97137009; PubMed=8982386;
RT  Nakamura T., Katoh Y., Shimizu Y., Matsuda Y., Unemoto T.;
RT  "Cloning and sequencing of novel genes from Vibrio alginolyticus that
RT  support the growth of K+ uptake-deficient mutant of Escherichia
RT  coli."
RL  Biochim. Biophys. Acta 1277:201-208(1996).
CC  -1- SIMILARITY: BELONGS TO THE UPF0001 FAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  DR  EMBL: D50472; BAA09062.1; -.
CC  DR  HSSP: P38197; 1B54.
CC  DR  InterPro: IPR001608; UPF0001.
CC  DR  Pfam: PF01168; UPF0001.1.
CC  DR  PROSITE: PS01211; UPF0001.1.
CC  KW  Hypothetical protein.
SQ  SEQUENCE 233 AA; 26049 MW; 4BEDBC17565CAFC CRC64;

Query Match          84.6%; Score 33; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2 NDORPS 7
    |||||
DB  114 NDORPS 119

RESULT 3
ASTB_FCOLI
ID  ASTB_ECOLI          STANDARD;          PRT;          447 AA.
AC  P76216;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Succinylarginine dihydrolase (EC 3.-.-.-).
GN  ASTB OR B1745.
OS  Escherichia coli.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Escherichia.
OX  NCBI_TaxID=562;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=K12 / MG1655;
RA  MEDLINE=97426617; PubMed=9278503;
RA  Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA  Blythe R., Daniels R., Glasner J.D., Rode C.K., Mayhew G.F.,
RA  Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA  Mau B., Shao Y.;
RT  "The complete genome sequence of Escherichia coli K-12.";
RT  Science 277:1453-1474(1997).
RL  [2]
CC  FUNCTION:
CC  MEDLINE=98361920; PubMed=9696779;
CC  Schneider B.L., Klupakis A.K., Reitzer L.J.;
CC  "Arginine catabolism and the arginine succinyltransferase pathway in
CC  Escherichia coli.";
CC  J. Bacteriol. 180:4278-4286(1998).
CC  -1- FUNCTION: CATALYZES THE HYDROLYSIS OF N(2)-SUCCINYLIARGININE INTO
CC  N(2)-SUCCINYLDORNITHINE, AMMONIA AND CO(2).
CC  -1- PATHWAY: SECOND STEP IN ARGININE CATABOLISM BY THE ARGININE

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CC  SUCCINYLTRANSFERASE PATHWAY.
CC  -----
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CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  DR  EMBL: AE000269; AAC74815.1; -.
CC  DR  EcGene: EG13996; astb.
CC  KW  Arginine metabolism; Hydrolase; Complete proteome.
CC  SEQUENCE 447 AA; 49298 MW; 710AB691E413AF64 CRC64;

Query Match          84.6%; Score 33; DB 1; Length 447;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY  1 GNDORPS 7
    |||||
DB  201 GNDORPS 207

RESULT 4
FMN_CHICK
ID  FMN_CHICK          STANDARD;          PRT;          1213 AA.
AC  Q05858;
DT  01-JUN-1994 (Rel. 29, Created)
DT  01-JUN-1994 (Rel. 29, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Formin (limb deformity protein).
GN  ID.
OS  Gallus gallus (chicken).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC  Gallus.
OX  NCBI_TaxID=9031;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=WHITE LEGHORN; TISSUE=embryo;
RA  MEDLINE=92112031; PubMed=1730407;
RA  Trump A., Blundell P.A., de la Pompa J.L., Zeller R.;
RT  "The chicken limb deformity gene encodes nuclear proteins expressed
RT  in specific cell types during morphogenesis.";
RL  Genes Dev. 6:14-28(1992).
CC  -1- FUNCTION: IS IMPORTANT FOR MORPHOGENESIS OF LIMB AND KIDNEY AND
CC  MAY BE INVOLVED IN DETERMINING DORSOVENTRAL NEURAL TUBE POLARITY
CC  AND MOTOR NEURON INDUCTION. IT MAY ALSO HAVE A FUNCTION IN
CC  DIFFERENTIATED CELLS OR BE INVOLVED IN MAINTAINING SPECIFIC
CC  DIFFERENTIATED STATES.
CC  -1- SUBCELLULAR LOCATION: Nuclear.
CC  -1- ALTERNATIVE PRODUCTS: MANY DIFFERENT FORMS OF THIS PROTEIN ARE
CC  PRODUCED BY ALTERNATIVE SPLICING OF THE LD GENE. A VARIATION
CC  IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND DIFFERENT SIZE
CC  TRANSCRIPTS EXIST WITHIN ANY ONE TISSUE.
CC  -1- TISSUE SPECIFICITY: PRESENT IN THE ADULT BRAIN, KIDNEY,
CC  BRAIN, HEART AND INTESTINE AND THROUGHOUT THE EMBRYO.
CC  -1- DEVELOPMENTAL STAGE: IN THE DEVELOPING LIMB BUD, THE PROTEIN IS
CC  EXPRESSED IN THE APICAL ECTODERMAL RIDGE AND THE MESENCHYMAL
CC  COMPARTMENT, PREDOMINANTLY IN THE POSTERIOR RESTRICTED TO
CC  THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS AND MESONEPHROS.
CC  -1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 1 (FH1) DOMAIN.
CC  -1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 2 (FH2) DOMAIN.
CC  -1- SIMILARITY: BELONGS TO THE FORMIN HOMOLOG FAMILY. CAPPUCCINO
CC  SUBFAMILY.
CC  -----
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:24 ; Search time 194.32 Seconds

(without alignments)
6.232 Million cell updates/sec

Title: US-09-780-035-29_COPY_51_57
Sequence: 39
1 GNDQPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP rvirus:*
16: SP bacteriap:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	84.6	395	3	09P3J2
2	33	84.6	544	2	09AQN0
3	33	84.6	1087	5	096923
4	32	82.1	339	10	0949T9
5	32	82.1	340	16	099X44
6	32	82.1	341	16	09CJDI
7	32	82.1	347	10	091Y92
8	32	82.1	362	2	057210
9	32	82.1	387	5	09VZX1
10	31	79.5	326	16	09HZN5
11	31	79.5	346	11	09CYG2
12	31	79.5	346	11	09DC33
13	31	79.5	364	2	091A57
14	31	79.5	402	10	082170
15	31	79.5	412	16	0990G6
16	31	79.5	417	4	09NMV2

17	31	79.5	417	4	09H9Y5	09H9Y5 homo sapien
18	31	79.5	417	4	09N232	09N232 homo sapien
19	31	79.5	500	2	093FS7	093FS7 cowdria rum
20	31	79.5	533	2	09JN10	09JN10 agrobacteri
21	31	79.5	868	5	09V7X8	09V7X8 drosophila
22	31	79.5	920	2	09KM05	09KM05 bacillus su
23	31	79.5	1036	5	09V9R1	09V9R1 drosophila
24	31	79.5	1148	16	09KM04	09KM04 bacillus su
25	31	79.5	1660	2	09EVR7	09EVR7 xenorhabdus
26	30	76.9	55	12	09PY44	09PY44 paramecium
27	30	76.9	109	12	084646	084646 paramecium
28	30	76.9	169	12	0917T3	0917T3 paramecium
29	30	76.9	169	12	0917T2	0917T2 paramecium
30	30	76.9	169	12	0917P3	0917P3 paramecium
31	30	76.9	171	17	09HPT3	09HPT3 halobacteri
32	30	76.9	186	12	091XZ1	091XZ1 halobacteri
33	30	76.9	186	12	091XZ0	091XZ0 halobacteri
34	30	76.9	186	12	091XY9	091XY9 halobacteri
35	30	76.9	186	12	091XY8	091XY8 halobacteri
36	30	76.9	186	12	091XY7	091XY7 halobacteri
37	30	76.9	186	12	091XY6	091XY6 halobacteri
38	30	76.9	186	12	091XY5	091XY5 halobacteri
39	30	76.9	186	12	091XY4	091XY4 halobacteri
40	30	76.9	186	12	091XY3	091XY3 halobacteri
41	30	76.9	186	12	091XY2	091XY2 halobacteri
42	30	76.9	186	12	091XY1	091XY1 halobacteri
43	30	76.9	186	12	091XY0	091XY0 halobacteri
44	30	76.9	186	12	091XX9	091XX9 halobacteri
45	30	76.9	186	12	091XX8	091XX8 halobacteri

ALIGNMENTS

RESULT 1
ID 09P3J2 PRELIMINARY: PRT: 395 AA.
AC 09P3J2:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE RELATED TO HYDROXYMETHYLGLUTARYL-COA LYASE.
GN B7F21.20.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP Schulte U., Algn V., Hohnsels J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Meeres H.W., Mannhaupt G.;
RN Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL389901; CAB97474.1;
DR InterPro; IPR008911; HMGL-1like.
KW Pfam; PF00682; HMGL-1like; 1.
KW Lyase.
SQ SEQUENCE 395 AA; 42464 MW; 32EAE8D9B0C332B5 CRC64;

Query Match 84.6%; Score 33; DB 3; Length 395;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NDQPS 7
Db 40 NDQPS 45
RESULT 2

09A0N0 PRELIMINARY; PRT; 544 AA.
 ID 09A0N0;
 AC 09A0N0;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOThETICAL 57.0 KDA PROTEIN.
 OS Pseudomonas sp. CA10.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=135214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CA10;
 RX MEDLINE=21264379; PubMed=11371531;
 RA Nojiri H., Sekiguchi H., Maeda K., Urata M., Nakai S., Yoshida T.,
 RA Haba H., Omori T.;
 RT "Genetic characterization and evolutionary implications of car gene
 RT cluster in carbazole-degrader, Pseudomonas sp. strain CA10.";
 RL J. Bacteriol. 183:3663-3679(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CA10;
 RX MEDLINE=97386424; PubMed=9244273;
 RA Sato S., Onchiyama N., Kimura T., Nojiri H., Yamane H., Omori T.;
 RT "Cloning of genes involved in carbazole degradation of Pseudomonas sp.
 RT strain CA10: nucleotide sequence of genes and characterization of
 RT meta-cleavage enzymes and hydrolase.";
 RL J. Bacteriol. 179:4841-4849(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CA10;
 RX MEDLINE=97386425; PubMed=9244274;
 RA Sato S., Nam J., Kasuga K., Nojiri H., Yamane H., Omori T.;
 RT "Identification and characterization of genes encoding carbazole 1,9a-
 RT dioxygenase in Pseudomonas sp. strain CA10.";
 RL J. Bacteriol. 179:4850-4858(1997).
 DR EMBL: AB047548; BAB32758.1; -
 DR InterPro: IPR002965; Pfich_extensin.
 DR PRINTS: PR01217; PRICHEXTENSIN.
 KW Hypothetical protein.
 SQ SEQUENCE 544 AA; 57043 MW; 0B316171518AF04A CRC64;

Query Match 84.6%; Score 33; DB 2; Length 544;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NDORPS 7
 |||||
 Db 143 NDORPS 148

RESULT 3
 096923 PRELIMINARY; PRT; 1087 AA.
 ID 096923;
 AC 096923;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GELSOLIN-RELATED PROTEIN GRP125.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX2;
 RX MEDLINE=99096692; PubMed=9880334;
 RA Stocker S., Hiery M., Marriott G.;
 RT "Phototactic migration of dictyostelium cells is linked to a new type
 RT of gelsolin-related protein.";
 RL Mol. Biol. Cell 10:161-178(1999).
 DR EMBL: U95159; AAD00774.1; -;

DR InterPro: IPR001974; Gelsolin.
 DR Pfam: PF00626; Gelsolin; 1.
 DR PRINTS: PR00597; GELSOLIN.
 DR SMART: SM00262; GEL_5
 SO SEQUENCE 1087 AA; 124777 MW; 8C431F5A0B51E677 CRC64;

Query Match 84.6%; Score 33; DB 5; Length 1087;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NDORPS 7
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 Db 670 NDORPS 675

RESULT 4
 0949T9 PRELIMINARY; PRT; 339 AA.
 ID 0949T9;
 AC 0949T9;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOThETICAL 38.3 KDA PROTEIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
 RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
 RA Carrinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kanuya A., Karlin-Neumann G., Kawai J., Kim C., Koeseke E., Lam B.,
 RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
 RA Shiozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene F18022_160/At5g14370 (GI:7573462).";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY050892; AAK92829.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 339 AA; 38276 MW; C911519472E0AD30 CRC64;

Query Match 82.1%; Score 32; DB 10; Length 339;
 Best Local Similarity 85.7%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNDORPS 7
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 Db 222 GNDORPS 228

RESULT 5
 099XH4 PRELIMINARY; PRT; 340 AA.
 ID 099XH4;
 AC 099XH4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE TRYPTOPHANYL-TRNA SYNTHETASE (EC 6.1.1.2).
 GN TRSA OR SPY2207.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
 RX MEDLINE=21192684; PubMed=11296296;
 DR Ferretti J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:48 ; Search time 84.18 Seconds

(without alignments)
2.031 Million cell updates/sec

File: US-09-780-035-29_COPY_51_57

Perfect score: 39

Sequence: 1 GNDQPS 7

Scoring table: BLOSUM62

Searched: GAPDP 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/1aa/3B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/3A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/3B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/3C.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/3D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	84.6	111	2	US-08-665-202-40
2	30	76.9	132	2	US-08-345-321-4
3	30	76.9	140	4	US-08-485-355B-44
4	30	76.9	311	3	US-08-911-423-8
5	30	76.9	384	2	US-08-673-388-11
6	30	76.9	384	2	US-08-614-877-11
7	29	74.4	24	4	US-08-778-865-51
8	29	74.4	26	4	US-07-942-245-230
9	29	74.4	26	4	US-08-602-999A-51
10	29	74.4	106	1	US-08-326-117B-9
11	29	74.4	106	1	US-08-326-117B-9
12	29	74.4	159	3	US-08-821-129-9
13	29	74.4	159	3	US-08-821-129-9
14	29	74.4	226	1	US-08-360-103A-4
15	29	74.4	226	1	US-08-360-103A-4
16	29	74.4	239	2	US-08-712-709-7
17	29	74.4	239	2	US-08-712-709-7
18	29	74.4	239	2	US-09-295-068-3
19	29	74.4	239	3	US-09-111-444-7
20	29	74.4	239	4	US-09-541-228-7
21	29	74.4	348	1	US-08-504-511A-2
22	29	74.4	348	1	US-08-504-511A-2
23	29	74.4	390	3	US-08-650-766-7
24	29	74.4	390	3	US-08-650-766-7
25	29	74.4	430	1	US-08-035-392-4
26	29	74.4	430	1	US-08-035-392-4
27	29	74.4	651	3	US-08-504-511A-4
28	29	74.4	651	3	US-08-504-511A-4
29	29	74.4	651	3	US-08-650-766-6
30	29	74.4	651	3	US-08-650-766-6
31	29	74.4	651	3	US-08-922-635-5
32	29	74.4	651	3	US-08-922-635-5
33	29	74.4	1056	2	US-08-687-289A-7
34	29	74.4	1056	2	US-08-687-289A-7
35	29	74.4	1056	2	US-08-687-289A-8
36	29	74.4	1056	2	US-08-687-289A-8
37	29	74.4	1056	2	US-08-687-289A-5
38	29	74.4	1056	2	US-08-687-289A-5
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43	29	74.4	1056	2	US-08-484-565-7
44	29	74.4	1056	2	US-08-484-565-7
45	29	74.4	1056	2	US-08-480-751-7
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47	29	74.4	1056	2	US-08-943-986-7
48	29	74.4	1056	2	US-08-943-986-7
49	29	74.4	1056	2	US-08-353-784-7
50	29	74.4	1056	2	US-08-353-784-7
51	29	74.4	1056	2	US-08-484-719B-7
52	29	74.4	1056	2	US-08-484-719B-7
53	29	74.4	1056	2	US-08-484-159-7
54	29	74.4	1056	2	US-08-484-159-7
55	29	74.4	1056	2	US-08-485-588-6
56	29	74.4	1056	2	US-08-485-588-6
57	29	74.4	1056	2	US-08-484-159-7
58	29	74.4	1056	2	US-08-484-159-7
59	29	74.4	1056	2	US-08-484-159-6
60	29	74.4	1056	2	US-08-484-159-6
61	29	74.4	1056	2	US-08-484-159-6
62	29	74.4	1056	2	US-08-484-159-6
63	29	74.4	1056	2	US-08-484-159-6
64	29	74.4	1056	2	US-08-484-159-6
65	29	74.4	1056	2	US-08-484-159-6
66	29	74.4	1056	2	US-08-484-159-6
67	29	74.4	1056	2	US-08-484-159-6
68	29	74.4	1056	2	US-08-484-159-6
69	29	74.4	1056	2	US-08-484-159-6
70	29	74.4	1056	2	US-08-484-159-6
71	29	74.4	1056	2	US-08-484-159-6
72	29	74.4	1056	2	US-08-484-159-6
73	29	74.4	1056	2	US-08-484-159-6
74	29	74.4	1056	2	US-08-484-159-6
75	29	74.4	1056	2	US-08-484-159-6
76	29	74.4	1056	2	US-08-484-159-6
77	29	74.4	1056	2	US-08-484-159-6
78	29	74.4	1056	2	US-08-484-159-6
79	29	74.4	1056	2	US-08-484-159-6
80	29	74.4	1056	2	US-08-484-159-6
81	29	74.4	1056	2	US-08-484-159-6
82	29	74.4	1056	2	US-08-484-159-6
83	29	74.4	1056	2	US-08-484-159-6
84	29	74.4	1056	2	US-08-484-159-6
85	29	74.4	1056	2	US-08-484-159-6
86	29	74.4	1056	2	US-08-484-159-6
87	29	74.4	1056	2	US-08-484-159-6
88	29	74.4	1056	2	US-08-484-159-6
89	29	74.4	1056	2	US-08-484-159-6
90	29	74.4	1056	2	US-08-484-159-6
91	29	74.4	1056	2	US-08-484-159-6
92	29	74.4	1056	2	US-08-484-159-6
93	29	74.4	1056	2	US-08-484-159-6
94	29	74.4	1056	2	US-08-484-159-6
95	29	74.4	1056	2	US-08-484-159-6
96	29	74.4	1056	2	US-08-484-159-6
97	29	74.4	1056	2	US-08-484-159-6
98	29	74.4	1056	2	US-08-484-159-6
99	29	74.4	1056	2	US-08-484-159-6
100	29	74.4	1056	2	US-08-484-159-6

ALIGNMENTS

28	29	74.4	1056	2	US-08-687-289A-8	Sequence 8, Appl
29	29	74.4	1056	2	US-08-687-289A-5	Sequence 5, Appl
30	29	74.4	1056	2	US-08-922-635-22	Sequence 2, Appl
31	29	74.4	1056	2	US-08-485-588-7	Sequence 7, Appl
32	29	74.4	1056	2	US-08-484-565-7	Sequence 7, Appl
33	29	74.4	1056	2	US-08-480-751-7	Sequence 7, Appl
34	29	74.4	1056	2	US-08-943-986-7	Sequence 7, Appl
35	29	74.4	1056	2	US-08-353-784-7	Sequence 7, Appl
36	29	74.4	1056	2	US-08-484-719B-7	Sequence 7, Appl
37	29	74.4	1056	2	US-08-484-159-7	Sequence 7, Appl
38	29	74.4	1056	2	US-08-485-588-6	Sequence 6, Appl
39	29	74.4	1056	2	US-08-484-159-7	Sequence 6, Appl
40	29	74.4	1056	2	US-08-485-588-6	Sequence 6, Appl
41	29	74.4	1056	2	US-08-943-986-6	Sequence 6, Appl
42	29	74.4	1056	2	US-08-353-784-6	Sequence 6, Appl
43	29	74.4	1056	2	US-08-484-719B-6	Sequence 6, Appl
44	29	74.4	1056	2	US-08-484-159-6	Sequence 6, Appl
45	29	74.4	1528	1	US-08-326-117B-2	Sequence 2, Appl

RESULT 1
US-08-665-202-40
Sequence 40, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-40
Query Match 84.6%, Score 33, DB 2, Length 111;

Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NDORPS 7
111111
Db 52 NDORPS 57

RESULT 2

US-08-345-321-4
; Sequence 4, Application US/08345321
; Patent No. 5914109
; GENERAL INFORMATION:
; APPLICANT: ZOLLA-PAZNER, Susan
; APPLICANT: GORNY, Mirosław K.
; TITLE OF INVENTION: HETEROHYBRIDOMAS PRODUCING HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO HIV-1
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/345,321
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,675
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: ZOLLA-PAZNER1B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-345-321-4

Query Match 76.9%; Score 30; DB 2; Length 132;
Best Local Similarity 71.4%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNDORPS 7
111111
Db 70 GNDORPS 76

RESULT 3

US-08-485-355B-44
; Sequence 44, Application US/08485355B
; Patent No. 6177075
; GENERAL INFORMATION:
; APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
; TITLE OF INVENTION: Insect Viruses and Their Uses in
; Protecting Plants
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr Hobach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,355B
FILING DATE: 07-Jun-1995
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Trecautlin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-2/REF/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-08-485-355B-44

Query Match 76.9%; Score 30; DB 4; Length 140;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNDORP 6
111111
Db 117 GSDORP 122

RESULT 4

US-08-911-423-8
; Sequence 8, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION: 336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
TELEFAX: 650-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-911-423-8

Query Match 76.9%; Score 30; DB 3; Length 311;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNDORP 6
1:||||
DB 302 GSDORP 307

RESULT 5
US-08-673-388-11
Sequence 11, Application US/08673388
Patent No. 5958745
GENERAL INFORMATION:
APPLICANT: Gruys, Kenneth J.
APPLICANT: Mitsky, Timothy A.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Slater, Steven C.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stark, David M.
APPLICANT: Hincbee, Maud A. W.
APPLICANT: Clemente, Thomas E.
APPLICANT: Connor-Ward, Dannelle V.
APPLICANT: Fedele, Mary J.
APPLICANT: Fry, Joyce E.
APPLICANT: Howe, Arlene R.
APPLICANT: Rozman, Renee J.
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and
TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
TITLE OF INVENTION: in Bacteria and Plants
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5958745th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,388
FILING DATE: 13-MAR-1996
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(13618)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-673-388-11

Query Match 76.9%; Score 30; DB 2; Length 384;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNDORP 6
1:||||
DB 74 GDDORP 79

RESULT 6
US-08-614-877-11
Sequence 11, Application US/08614877
Patent No. 5959179
GENERAL INFORMATION:
APPLICANT: Gruys, Kenneth J.
APPLICANT: Mitsky, Timothy A.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Slater, Steven C.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stark, David M.
APPLICANT: Hincbee, Maud A. W.
APPLICANT: Clemente, Thomas E.
APPLICANT: Connor-Ward, Dannelle V.
APPLICANT: Fedele, Mary J.
APPLICANT: Fry, Joyce E.
APPLICANT: Howe, Arlene R.
APPLICANT: Rozman, Renee J.
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and
TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval
TITLE OF INVENTION: in Bacteria and Plants
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5959179th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,877
FILING DATE: 13-MAR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10695)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 384 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-614-877-11

Query Match 76.9%; Score 30; DB 2; Length 384;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNDORP 6
1:||||
DB 74 GDDORP 79

RESULT 7
US-08-278-865-51
Sequence 51, Application US/08278865
Patent No. 6303574
GENERAL INFORMATION:
APPLICANT: SPARKS, BRIAN K.
APPLICANT: THORN, JUDITH M.
APPLICANT: OULLIAM, LAWRENCE A.
APPLICANT: DER, CHANNING J.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,865
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-007-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-278-865-51

Query Match 74.4%; Score 29; DB 4; Length 24;
Best Local Similarity 71.4%; Pred. No. 8; 8;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNDORP 7
1:||||
DB 17 GHDSRS 23

RESULT 8
US-07-942-245-230
Sequence 230, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-230

Query Match 74.4%; Score 29; DB 1; Length 26;
Best Local Similarity 83.3%; Pred. No. 9.6;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GNDORP 6
1:||||
DB 19 GNSORP 24

RESULT 9
US-08-602-999A-51
Sequence 51, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OULLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana E.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-51

Query Match 74.4%; Score 29; DB 4; Length 26;
Best Local Similarity 71.4%; Pred. No. 9.6;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GNDPRS 7
1:|||||
Db 19 GHDSRPS 25

RESULT 10
US-08-326-117B-9
; Sequence 9, Application us/08326117B
; Patent No. 5693491
; GENERAL INFORMATION:
; APPLICANT: BULLA, LEE A.
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; TITLE OF INVENTION: TOXIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,117B
; FILING DATE: 19-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36, 217
; REFERENCE/DOCKET NUMBER: 7112-0037.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid

STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-326-117B-9

Query Match 74.4%; Score 29; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NDORP 6
|||||
Db 100 NDORP 104

RESULT 11
US-08-982-129-9
; Sequence 9, Application US/08982129
; Patent No. 6007981
; GENERAL INFORMATION:
; APPLICANT: BULLA, LEE A.
; TITLE OF INVENTION: RECEPTOR FOR A BACILLUS THURINGIENSIS
; TITLE OF INVENTION: TOXIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,129
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/326,117
; FILING DATE: 19-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36, 217
; REFERENCE/DOCKET NUMBER: 7112-0037.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-982-129-9

Query Match 74.4%; Score 29; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NDORP 6
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Db 100 NDORP 104

RESULT 12
US-08-415-655-7
; Sequence 7, Application US/08415655
; Patent No. 6025480

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,103A
FILING DATE: 20-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93.203.584.3
FILING DATE: 20-DEC-1993
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acids
Type: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-360-103A-4

Query Match          74.4%; Score 29; DB 1; Length 226;
Best Local Similarity 83.3%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GNDQRP 6
        |||||
Db       22 GNDQAP 27

RESULT 14
US-08-712-709-7
; Sequence 7, Application US/08712709
; Patent No. 5863780
;
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
Type: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptid
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1082115
US-08-712-709-7

Query Match          74.4%; Score 29; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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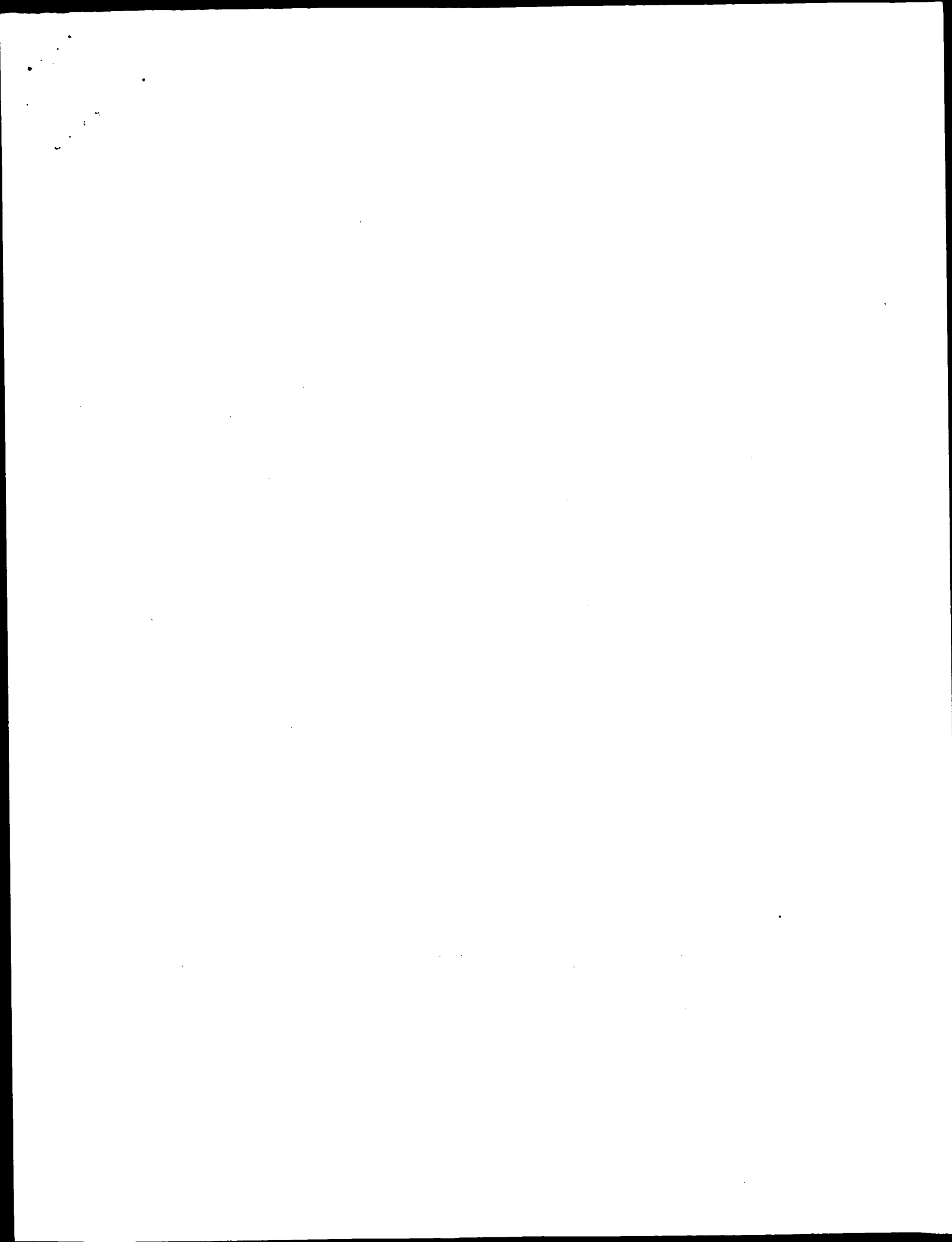

OY 2 NDORP 6
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Db 226 NDORP 230

RESULT 15

US-09-049-671-3
; Sequence 3, Application US/09049671
; Patent No. 5928874
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Marian
; TITLE OF INVENTION: NEKI-RELATED PROTEIN KINASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,671
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0492 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1082115
; US-09-049-671-3

Query Match 74.4%; Score 29; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 NDORP 6
|||||
Db 226 NDORP 230

Search completed: June 21, 2002, 09:21:49
Job time: 412 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:18 ; Search time 245.49 Seconds

(Without alignments)
4.977 Million cell updates/sec

Title: US-09-780-035-29_COPY_90_100
Perfect score: 60
Sequence: 1 AAMDSLSGPV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDSI/gcgcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	60	100.0	11	22	AAG65315	Anti-IL-18 antilbod
2	60	100.0	111	22	AAG65319	Anti-IL-18 antilbod
3	60	100.0	111	22	AAG65355	Anti-IL-18 antilbod
4	60	100.0	235	22	AAG65320	Anti-IL-18 antilbod
5	60	100.0	236	22	ABG23083	Novel human diagno
6	57	95.0	111	18	AAW13519	Anti-melanoma ligh
7	57	95.0	153	21	AAW53653	Human colon cancer
8	53	88.3	119	22	ABW31633	Peptide #4284 enco
9	53	88.3	119	22	ABW22173	Protein #4172 enco
10	53	88.3	119	22	AAW69997	Human bone marrow
11	53	88.3	237	22	ABG19300	Novel human diagno

12	51	85.0	113	14	AAW34277	Human Vlamdab1-1-1
13	50	83.3	271	20	AAW90180	Human Clone A6 fus
14	49	81.7	11	20	AAW90299	Human anti-GPIIb/I
15	49	81.7	98	14	AAW34275	Human TNF binding
16	49	81.7	98	21	AAW40145	Anti-IL12 antilbod
17	49	81.7	109	21	AAW95205	Anti-platelet glyc
18	49	81.7	109	22	AAW95616	Human anti-Rh(D) c
19	49	81.7	111	18	AAW08492	C6 human sfv antib
20	49	81.7	111	20	AAW90279	Human anti-GPIIb/I
21	49	81.7	112	18	AAW08488	C6 human sfv antib
22	49	81.7	113	14	AAW34276	Human Vlamdab1-1-1
23	49	81.7	113	14	AAW34278	Human Vlamdab1-1-1
24	49	81.7	258	18	AAW08487	C6 human sfv antib
25	49	81.7	262	20	AAW97890	C6.5/218 single ch
26	48	80.0	190	22	ABG26351	Novel human diagno
27	48	80.0	687	21	AAW50835	Arabidopsis thalia
28	48	80.0	689	21	AAW50834	Arabidopsis thalia
29	48	80.0	707	21	AAW50833	Arabidopsis thalia
30	47	78.3	109	22	AAW93812	Human anti-Rh(D) c
31	47	78.3	111	17	AAW88506	Vlamdab1 for antib
32	47	78.3	118	22	AAW65555	Amino acid sequenc
33	47	78.3	132	22	AAW65561	Novel human diagno
34	47	78.3	353	22	ABG26353	Novel human diagno
35	46	76.7	11	20	AAW90300	Human anti-GPIIb/I
36	46	76.7	98	21	AAW40144	Anti-IL12 antilbod
37	46	76.7	98	21	AAW40146	Anti-IL12 antilbod
38	46	76.7	111	18	AAW08489	C6 human sfv antib
39	46	76.7	111	18	AAW08491	C6 human sfv antib
40	46	76.7	111	20	AAW90281	Human anti-GPIIb/I
41	46	76.7	235	20	AAW88465	Monoclonal antilbod
42	46	76.7	248	22	ABG26352	Novel human diagno
43	45	75.0	11	22	AAW62992	Complementarity de
44	45	75.0	109	22	AAW93613	Human anti-Rh(D) c
45	45	75.0	110	22	AAW93617	Human anti-Rh(D) c

ALIGNMENTS

```

RESULT 1
AAG65315
ID AAG65315 standard; protein; 11 AA.
AC AAG65315;
XX
XX 30-NOV-2001 (first entry)
XX
DE Anti-IL-18 antibody LT28 light chain CDR3 fragment.
XX
XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
XX KW nootropic; neurologic; antiinflammatory; antiparkinsonian; cardiant;
XX KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
XX
XX Homo sapiens.
XX PN WO200158956-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-0504170.
XX
XX 10-FEB-2000; 2000US-0181608.
XX
XX (BADI ) BASF AG.
XX
XX Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J,
XX Duncan AR, Brocklehurst SM, Mankovich J, Shortrock CP, Thompson JE,
XX Leonard SN;
XX WPI; 2001-550020/61.
XX
XX Novel antibodies and compounds capable of binding to human
XX interleukin-18 useful for treating, e.g., inflammatory disorders,
XX

```

PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX Claim 34; Page 42; 91pp; English.
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LT28
 CC light chain CDR3 fragment.
 CC Sequence 11 AA;
 XX
 QY 1 AAWDSLSPV 11
 Db 1 aawdslspv 11
 Query Match 100.0%; Score 60; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 AAG65319
 ID AAG65319 standard; protein; 111 AA.
 XX
 AC AAG65319;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Anti-IL-18 antibody LT28 light chain sequence.
 XX
 KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI: 2001-550020/61.
 DR N-PSDB; AAH47514.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX Claim 36; Page 42; 91pp; English.

XX
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a
 CC disorder where IL-18 is detrimental in, a human subject suffering from,
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
 CC antibody may occur before, concurrent, or after administration of a
 CC second agent selected from an antibody, or fragment, capable of binding
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
 CC agents. The present sequence represents an anti-IL-18 antibody LT28
 CC light chain sequence.
 CC Sequence 111 AA;
 XX
 QY 1 AAWDSLSPV 11
 Db 90 aawdslspv 100
 Query Match 100.0%; Score 60; DB 22; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 AAG65355
 ID AAG65355 standard; protein; 111 AA.
 XX
 AC AAG65355;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Anti-IL-18 antibody LT28 light chain sequence.
 XX
 KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
 KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac;
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic; LT28.
 XX
 OS Homo sapiens.
 XX
 PN WO200158956-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US04170.
 XX
 PR 10-FEB-2000; 2000US-0181608.
 XX
 PA (BADI) BASF AG.
 XX
 PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
 PI Lennard SN;
 XX
 DR WPI: 2001-550020/61.
 DR N-PSDB; AAH47514.
 XX
 PT Novel antibodies and compounds capable of binding to human
 PT interleukin-18 useful for treating, e.g., inflammatory disorders,
 PT neurological disorders, heart failure, myocardial infarction, and
 PT autoimmune diseases -
 XX Example 2; Page 90; 91pp; English.
 XX
 CC The invention provides isolated antibodies, or antigen-binding portions,
 CC that are capable of binding to human interleukin-18 (IL-18). The
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a

CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 236 AA;

Query Match

Best Local Similarity 100.0%; Score 60; DB 22; Length 236;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLGPV 11
 DB 110 aawdslgvpv 120

RESULT 6

AAW13519 standard; protein; 111 AA.

XX AAW13519;

DT 28-OCT-1997 (first entry)

DE Anti-melanoma light chain antibody clone 278.

KW Human: monoclonal antitumour antibody; peripheral blood lymphocyte;

KW cancer; tumourigenesis; anticancer vaccine.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 23..35

FT Region /label= CDR1

FT Region 51..57

FT Region /label= CDR2

FT Region 90..99

FT Region /label= CDR3

XX WO9702479-A2.

XX 23-JAN-1997.

XX 28-JUN-1996; 96WO-IB01032.

XX 30-JUN-1995; 95US-0497647.

XX (UYVA) UNITV YALE.

XX Cai X, Garen A;

XX WPI; 1997-109061/10.

XX Prod. of human monoclonal anti-tumour antibodies - by screening a

XX fusion phage library produced using peripheral blood lymphocytes

XX from a cancer patient

XX Claim 19; Page 57; 82pp; English.

XX A process for isolating and synthesizing human monoclonal anti-tumour

XX antibodies has been produced. The process involves: (a) constructing at

XX least one fusion phage library from the peripheral blood lymphocytes in

XX (PBUs) of a cancer patient; (b) screening for anti-tumour antibodies in

XX the phage library in a binding assay with cultured tumour cells of the

XX same type as the patient's tumour; (c) removing extraneous antibodies by

XX absorption against normal human cells; (d) cloning the phage selected in

XX step (b) and (c); (e) assaying the specificity of the cloned phage by

XX incubating the phage with at least two types of cultured normal cells;

XX and (f) further testing the specificity of cloned phage that do not bind

CC to either cell line of cultured normal cells in further binding assays
 CC to cultured tumour cells derived from more than one other tumour that is
 CC not the patient's tumour. The present sequence represents a human light
 CC chain antibody, from an scFv antibody fusion phage library, produced by
 CC a method as described above. The antibodies produced can be used for
 CC diagnostic and therapeutic applications and for isolating tumour
 CC antigens for studying tumourigenesis or for use as anti-cancer vaccines.
 CC The human antibodies have low immunogenicity in humans compared to
 CC murine monoclonal antibodies (MAbs). Since the antibodies are isolated
 CC from fusion phage libraries, their affinity and specificity for a
 CC tumour cell line can be improved by genetic manipulations.

XX Sequence 111 AA;

Query Match

Best Local Similarity 90.9%; Score 57; DB 18; Length 111;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLGPV 11
 DB 90 aawdslgvpv 100

RESULT 7

AAB53653 standard; protein; 153 AA.

XX AAB53653;

DT 09-MAR-2001 (first entry)

DE Human colon cancer antigen protein sequence SEQ ID NO:1193.

KW Human; colon cancer; colon cancer antigen; diagnosis; detection;

KW identification; cytostatic; cardioactive; neuroprotective; vulnereary;

KW immunomodulatory; muscular; gynaecological; gastrointestinal;

KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;

KW neutral disorder; immune system disorder; muscular disorder;

KW reproductive disorder; gastrointestinal disorder; renal disorder;

XX Infectious disease; cardiovascular disorder.

XX Homo sapiens.

XX WO200055351-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05883.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587534/55.

XX N-PSDB; AAC98410.

XX Colon cancer associated gene sequences, referred to as colon cancer

XX antigens, useful for the treatment, prevention, and diagnosis of colon

XX disorders such as colon cancer

XX Claim 11; Page 1775-1776; 2104pp; English.

XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,

XX called human colon cancer antigens, given in AAB53234 to AAB54006. The

XX human colon cancer antigens can have cytostatic, cardioactive, muscular;

XX neuroprotective, immunomodulatory, gynaecological, gastrointestinal,

XX vulnereary, nephrotropic, antiinfective and antibacterial activities, and

XX can be used in gene therapy. The colon cancer antigen polynucleotides,

XX proteins and antibodies to the proteins are useful for the prevention,

XX treatment and diagnosis of colon disorders, such as colon cancer. The

CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins
CC may also be used to prevent diseases such as neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, wounds, renal disorders, infectious
CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC AAB54007 represent sequences used in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 153 AA;
XX
XX
Query Match 95.0%; Score 57; DB 21; Length 153;
Best Local Similarity 90.9%; Pred. No. 0.011;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDSLSPGV 11
117 aswdsdlsqpv 127
Db 117 aswdsdlsqpv 127
XX
XX
RESULT 8
AAB31633
ID ABB31633 standard; Peptide; 119 AA.
XX
XX ABB31633;
AC
XX 01-FEB-2002 (first entry)
DT
XX
XX Peptide #4284 encoded by breast cell single exon nucleic acid probe.
DE
XX
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer.
XX
XX Homo sapiens.
OS
XX WO200157271-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US00662.
PF
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-496933/54.
PT
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX
XX Claim 27; SEQ ID NO 14601; 327bp + sequence listing; English.
PS
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater

CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 119 AA;
XX
XX
Query Match 88.3%; Score 53; DB 22; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.044;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDSLSPGV 10
90 aswdsdlsngp 99
Db 90 aswdsdlsngp 99
XX
XX
RESULT 9
AAB22173
ID ABB22173 standard; Protein; 119 AA.
XX
XX ABB22173;
AC
XX 23-JAN-2002 (first entry)
DT
XX
XX Protein #4172 encoded by probe for measuring heart cell gene expression.
DE
XX
XX Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
XX Homo sapiens.
OS
XX WO200157274-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US00666.
PF
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488899/53.
PT
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
XX
XX Claim 15; SEQ ID NO 23943; 530bp; English.
PS
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABB2135-ABA11305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 119 AA;

Query Match 88.3%; Score 53; DB 22; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.044;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLSLGP 10
|||||:|
DB 90 aawdslingp 99

RESULT 10

AAM69997
ID AAM69997 standard; Protein: 119 AA.

AC AAM69997;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30303.

KW Human: bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

XX 09-AUG-2001.

PD 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 30303; 658bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX bone marrow. They can be used to measure gene expression in bone marrow

XX samples, which can enable the improved diagnosis and treatment of cancers

XX such as lymphoma, leukaemia and myeloma. The present sequence is a

XX protein encoded by one of the probes of the invention.

SQ Sequence 119 AA;

Query Match 88.3%; Score 53; DB 22; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.044;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLSLGP 10
|||||:|
DB 90 aawdslingp 99

RESULT 11

ABG19300
ID ABG19300 standard; Protein: 237 AA.

XX ABG19300;

XX 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #19291.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

PN WO200175067-A2.

XX 11-OCT-2001.

PP 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS83487.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity -

XX Claim 20; SEQ ID NO 49659; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and

XX polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX and gene mapping, and in recombinant production of (II). The

XX polynucleotides are also used in diagnostics as expressed sequence tags

XX for identifying expressed genes. (I) is useful in gene therapy techniques

XX to restore normal activity of (II) or to treat disease states involving

XX (II). (II) is useful for generating antibodies against it, detecting or

XX quantitating a polypeptide in tissue, as molecular weight markers and as

XX a food supplement. (II) and its binding partners are useful in medical

XX imaging of sites expressing (II). (I) and (II) are useful for treating

XX disorders involving aberrant protein expression or biological activity.

XX The polypeptide and polynucleotide sequences have applications in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits to assess biodiversity

XX and to produce other types of data and products dependent on DNA and

XX amino acid sequences. ABG00010-ABG30377 represent novel human

XX diagnostic amino acid sequences of the invention.

Query Match 88.3%; Score 53; DB 22; Length 237;
Best Local Similarity 90.0%; Pred. No. 0.094;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLSLGP 10
|||||:|
DB 208 aawdslingp 217

RESULT 12


```

AAR34277
ID AAR34277 standard; Protein; 113 AA.
XX
AC AAR34277;
XX
DT 26-JUL-1993 (first entry)
XX
DE Human Vlamdbal-1-1 light chain derived clone Vlamdbac4.
XX
KW Monoclonal antibody; anti-globulin response; VL gene;
KW chimeric; mouse-human antibodies; antibody; prevention;
KW tumour necrosis factor.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Region 1..22
XX FT /note= "Framework region FR1"
XX FT 23..35
XX FT /note= "Complementarity determining region CDR1"
XX FT 36..50
XX FT /note= "Framework region FR2"
XX FT 51..57
XX FT /note= "Complementarity determining region CDR2"
XX FT 58..89
XX FT /note= "Framework region FR3"
XX FT 90..102
XX FT /note= "Complementarity determining region CDR3"
XX FT 103..113
XX FT /note= "Framework region FR4"
XX
XX PN WO9306213-A.
XX PD 01-APR-1993.
XX
XX PF 23-SEP-1992; 92WO-GB01755.
XX
XX PR 23-SEP-1991; 91GB-0020252.
XX PR 25-SEP-1991; 91GB-0020377.
XX PR 24-MAR-1992; 92GB-0006318.
XX PR 24-MAR-1992; 92GB-0006372.
XX PR 15-MAY-1992; 92WO-GB00883.
XX
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PA (MED-) MEDICAL RES COUNCIL.
XX
XX PI Baier M, Hoogenboom HRM, Jespers LSAT, Winter GP;
XX
XX WPI; 1993-117534/14.
XX
XX PT Producing human antibody polypeptide dimer specific for antigen -
XX FT comprises use of chain shuffling using phage expression, useful
XX FT for reducing anti globulin responses in humans for increased
XX FT human characteristics
XX
XX PS Example; Fig 6; 109pp; English.
XX
XX CC The sequence is that of the light chain clone Vlamdbac4 derived
XX CC from the Vlamdbal-1-1 germline human VL gene of antibody
XX CC fragments binding to human TNF. It has 1 amino-acid residue
XX CC different from the germline and may be used as part of a method
XX CC of producing chimeric mouse-human antibodies or fragments which
XX CC have the same binding specificity as a parent Ab but have increased
XX CC human characteristics, preventing anti-globulin response in humans.
XX
XX SQ Sequence 113 AA;

```

```

Db 90 aawdsglsgv 100
|||||||
|

RESULT 13
AAW90180
ID AAW90180 standard; Protein; 271 AA.
XX
AC AAW90180;
XX
DT 10-MAY-1999 (first entry)
XX
DE Human clone A6 fusion protein antibody.
XX
KW Antibody; human; clone A6; hab; fusion protein; polystyidine tag;
KW Western blot; enzyme-linked immunosorbent assay; ELISA; therapy;
KW immunofluorescence; immunoprecipitation assay; affinity purification;
KW diagnosis; vaccine; serum; immune response.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FT Protein 1..271
XX FT /note= "Partial coding sequence, no stop codon given"
XX
XX PN WO9901475-A2.
XX
XX PD 14-JAN-1999.
XX
XX PF 03-JUL-1998; 98WO-DE01882.
XX
XX PR 04-JUL-1997; 97DE-1028697.
XX
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX PI Braunagel M, Doersam H, Kipriyanov S, Kuerschner T;
XX PI Little M, Welschhof M;
XX
XX WPI; 1999-106000/09.
XX
XX DR N-PSDB; AAV74274.
XX
XX PT Human antibody against fusion protein with polystyidine tag -
XX FT useful as standard in immunoassays, for affinity purification,
XX FT diagnosis and therapy and for preparing vaccines
XX
XX PS Claim 2; Fig 4; 20pp; German.
XX
XX CC This invention describes a human antibody (hab) against a fusion
XX CC (poly)peptide or protein that includes a segment of at least 6
XX CC consecutive His residues. This antibody is useful in Western blots,
XX CC enzyme-linked immunosorbent assay (ELISA), immunofluorescence or
XX CC immunoprecipitation assays. Also hab can be used for affinity
XX CC purification of the protein, for in vivo diagnosis or therapy, and
XX CC in production of vaccines. hab are universally applicable
XX CC alternatives to human serum. They are specific for the polystyidine
XX CC tag, regardless of the nature of the rest of the protein. Since hab
XX CC are not produced in an animal, they contain no components that can
XX CC induce an immune response in humans.
XX
XX SQ Sequence 271 AA;

```

```

Query Match 85.0%; Score 51; DB 14; Length 113;
Best Local Similarity 90.9%; Pred. No. 0.097; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 AAWDLSLSPV 11

```

```

Query Match 83.3%; Score 50; DB 20; Length 271;
Best Local Similarity 90.9%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 AAWDLSLSPV 11
Db 232 aawdsglsgv 242
RESULT 14
AAW90299

```


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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:45 ; Search time 109.39 Seconds

(without alignments)
9.663 Million cell updates/sec

Title: US-09-780-035-29_COPY_90_100

Sequence: 1 AAMDLSGSPV 11

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	235	2	S25750 Ig lambda chain -
2	55	91.7	112	2	D44151 Ig lambda chain V-
3	52	86.7	111	1	LIHVOV Ig lambda chain V-
4	52	86.7	112	2	C44151 Ig lambda chain V-
5	49	81.7	98	2	S36048 Ig lambda chain -
6	49	81.7	112	2	B44151 Ig lambda chain V
7	49	81.7	129	2	S78058 Ig lambda chain pr
8	48	80.0	112	2	A44151 Ig lambda chain V
9	48	80.0	149	2	S23626 Ig lambda chain V
10	48	80.0	233	2	S25752 Ig lambda chain V
11	46	76.7	98	2	S36046 Ig lambda chain -
12	46	76.7	98	2	S36047 Ig lambda chain -
13	46	76.7	110	2	S57428 Ig light chain V-J
14	46	76.7	112	1	LIHVMW Ig lambda chain V-
15	46	76.7	117	2	S23627 Ig lambda chain pr
16	46	76.7	234	2	S25757 Ig lambda chain -
17	46	76.7	235	2	S25754 Ig lambda chain -
18	41	68.3	110	2	S36258 Ig lambda chain V
19	41	68.3	504	2	S46752 Ig lambda chain V
20	40	66.7	95	2	S49571 Ig lambda chain pr
21	40	66.7	130	2	S78057 Ig lambda chain pr
22	40	66.7	185	2	A49957 Ig lambda chain pr
23	40	66.7	197	2	S51372 CD45-associated 30
24	40	66.7	308	2	T46294 membrane protein L
25	40	66.7	355	2	E87394 conserved hypotet
26	40	66.7	759	2	AF0577 molycoprotein-cont
27	39	65.0	109	1	LIHUMA Ig lambda chain V-
28	39	65.0	110	2	S57408 Ig lambda chain V-
29	39	65.0	140	2	G96603 unknown protein F1

30	39	65.0	145	2	S25743 Ig lambda chain -
31	39	65.0	216	2	A42193 Ig lambda chain (B
32	39	65.0	535	2	D96586 hypothetical prote
33	39	65.0	1618	2	S21424 nestin - human
34	38	63.3	206	2	A83318 hypothetical prote
35	38	63.3	220	2	A83360 hypothetical prote
36	38	63.3	393	2	AF3619 probable cytochrom
37	38	63.3	585	2	T19814 hypothetical prote
38	38	63.3	929	2	T31462 hypothetical prote
39	38	63.3	1292	2	T31462 probable magnesium
40	38	63.3	1686	2	A87692 conserved hypotet
41	37	61.7	276	2	H81931 probable bis(5'-nu
42	37	61.7	320	2	A75278 probable cobw prot
43	37	61.7	357	2	S47402 outer membrane pro
44	37	61.7	365	2	E97484 outer membrane pro
45	37	61.7	365	2	AD2702 outer membrane pro

ALIGNMENTS

RESULT 1
S25750
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25750
R:Combiarto, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A:Reference number: S16459; MUID:91257162
A:Accession: S25750
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57815; NID:933729; PIDN:CAA0952.1; PID:933730
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 100.0%; Score 60; DB 2; Length 235;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAMDLSGSPV 11
DB 109 AAMDLSGSPV 119

RESULT 2
D44151
Ig lambda chain V region (BO-12) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: D44151
R:Zebedee, S.L.; Barbis III, C.F.; Hom, Y.L.; Caotien, R.H.; Graff, R.; Degraw, J.;
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:9228746
A:Accession: D44151
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-112 <ZEB>
A>Note: nucleotide translation is not given
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-90/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 91.7%; Score 55; DB 2; Length 112;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AAMDLSLGPV 11
|||||
Db 89 AAMDLSLGPV 99

RESULT 3

1 HV0
Ig lambda chain V-I region (Vor) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A01962
R:Engelhardt, M.; Hilschmann, N.
Hoppe-Seidler, S. Z. Physiol. Chem. 356, 1413-1444, 1975
A:Title: Pattern of antibody structure. The amino acid sequence of a monoclonal immunoglobulin of antibody specificity.
A:Reference number: A01962; MUID:76023790
A:Accession: A01962
A:Molecule type: protein
A:Residues: 1-111 <ENG>
A:Note: the C region of this chain has the Oz+ marker
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGLV6
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer
F:15-91/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status
F:2-89/Disulfide bonds: #status predicted

Query Match 86.7%; Score 52; DB 1; Length 111;
Best Local Similarity 81.8%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAMDLSLGPV 11
|||||
Db 90 AAMDLSLGPV 100

RESULT 4

C44151
Ig lambda chain V region (BO-10) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: C44151
R:Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caotchen, R.H.; Graff, R.; Degraw, J.; Pya
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746
A:Accession: C44151
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-112 <ZEB>
A:Note: nucleotide translation not given
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 86.7%; Score 52; DB 2; Length 112;
Best Local Similarity 90.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AAMDLSLGPV 11
|||||
Db 90 AAMDLSLGPV 99

RESULT 5
S36048
Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36048; S36049
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36048
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <WIL>
A:Cross-references: EMBL:222189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:2221
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLSLGPV 9
|||||
Db 90 AAMDLSLGPV 98

RESULT 6

B44151
Ig lambda chain V region (BO-09) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: B44151
R:Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caotchen, R.H.; Graff, R.; Degraw, J.;
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746
A:Accession: B44151
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA
A:Residues: 1-112 <ZEB>
A:Cross-references: GB:M88310; NID:g183954; PIDN:AAA35968.1; PID:g183955
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 49; DB 2; Length 112;
Best Local Similarity 80.0%; Pred. No. 0.13;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 AAMDLSLGPV 11
|||||
Db 90 AAMDLSLGPV 99

RESULT 7

S78058
Ig lambda chain precursor V-J region (clone mAb 67VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78058; S23723
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78058
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g9930121
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nock
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low an

OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE.
 RA MEDLINE=85257662; PubMed=2410269;
 RX Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
 RT "The amino acid sequence of a lambda light chain presenting abnormal
 RT physicochemical and antigenic features";
 RL Eur. J. Biochem. 150:349-357(1985).
 CC -1- MISCELLANEOUS: RESIDUES 33-36 AND SOME OF THE SEQUENCED PEPTIDES
 CC WERE POSITIONED BY HOMOLOG.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE MCG+ AND KERN+
 CC MARKERS.
 DR PIR: A25479; LIHUM.
 DR HSSP: P01703; 7FAB.
 DR InterPro: IPR003596; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IgV; 1.
 KM Immunoglobulin V region; Monoclonal antibody.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 90 BY SIMILARITY.
 FT NON_TER 112 112
 FT SEQUENCE 112 AA; 11789 MW; 748124F079CFFBE4 CRC64;

Query Match 76.7%; Score 46; DB 1; Length 112;
 Best Local Similarity 81.8%; Pred. No. 0.049;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAMDSDLGCV 11
 DB 91 AAMDSDLGCV 101

RESULT 3
 YHV9_YEAST
 ID YHV9_YEAST STANDARD: PRT: 504 AA.
 AC P38854;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Hypothetical 56.3 kDa protein in REC104-SOL3 intergenic region.
 GN YHR159W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RC MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favello A., Fulton L., Gatung S., Giesel C., Kirsten J.,
 RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
 RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
 RA Nham M., Rifkin L., Riles L., St Peter H., Trevasaki E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT VIII";
 RL Science 265:2077-2082(1994).
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: U010397; AAB68975.1; -
 CC PIR: S46752; S46752.
 DR SGD: S0001202; YHR159W.
 DR KW Hypothetical protein.

SO SEQUENCE 504 AA; 56313 MW; AEB8B94335D1DB63 CRC64;

Query Match 68.3%; Score 41; DB 1; Length 504;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WDDSLSG 9
 DB 332 WDDSLSG 338

RESULT 4
 LV1F_HUMAN
 ID LV1F_HUMAN STANDARD: PRT: 109 AA.
 AC P04208;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-1 region WAH.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE.
 RX MEDLINE=83221661; PubMed=6407018;
 RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
 RT "Complete covalent structure of a human immunoglobulin D: sequence of
 RT the lambda light chain";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
 DR PIR: A01967; LIHWA.
 DR HSSP: P01703; 7FAB.
 DR InterPro: IPR003596; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IgV; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 1 97 V SEGMENT.
 FT DOMAIN 98 109 J SEGMENT.
 FT DISULFID 22 89 BY SIMILARITY.
 FT NON_TER 109 109
 FT SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 65.0%; Score 39; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDSDL 7
 DB 90 AAMDSDL 96

RESULT 5
 NEST_HUMAN
 ID NEST_HUMAN STANDARD: PRT: 1618 AA.
 AC P48681; 000552;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Nestin.
 GN NES.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RC MEDLINE=93123384; PubMed=1478958;
 RA Dahlstrand J., McKay R.D.G., Zimmerman L.B., Lendahl U.;
 RT "Characterization of the human nestin gene reveals a close

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:25 ; Search time 194.32 Seconds

(without alignments)
9.793 Million cell updates/sec

Title: US-09-780-035-29_COPY_90_100
Perfect score: 60
Sequence: 1 AAMDSTLSGPV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP_rvirus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	73.3	108	4 Q96SBO	Q96SBO homo sapien
2	40	66.7	197	11 Q64697	Q64697 mus musculu
3	40	66.7	355	16 Q9A925	Q9A925 caulobacter
4	39	65.0	133	10 Q48629	Q48629 prunus arme
5	39	65.0	140	10 Q9C7J7	Q9C7J7 arabidopsis
6	39	65.0	430	4 Q9H6U9	Q9H6U9 homo sapien
7	39	65.0	535	10 Q9SLI8	Q9SLI8 arabidopsis
8	39	65.0	634	5 Q952I0	Q952I0 cuplenius
9	38	63.3	90	10 Q9LJG7	Q9LJG7 arabidopsis
10	38	63.3	139	4 Q9NPJ4	Q9NPJ4 homo sapien
11	38	63.3	206	16 Q9IOK6	Q9IOK6 pseudomonas
12	38	63.3	220	16 Q9I1J0	Q9I1J0 pseudomonas
13	38	63.3	244	7 Q3I358	Q3I358 brachydantio
14	38	63.3	267	2 Q93IW7	Q93IW7 streptomyce
15	38	63.3	585	2 Q45298	Q45298 caenorhabdi
16	38	63.3	614	5 Q46149	Q46149 platynereis

17	38	63.3	929	10 Q23410	Q23410 arabidopsis
18	38	63.3	1292	2 Q9ZGE5	Q9ZGE5 heliobacilli
19	38	63.3	1686	16 Q9A230	Q9A230 caulobacter
20	37	61.7	92	15 Q80334	Q80334 human immun
21	37	61.7	124	15 Q90B55	Q90B55 human immun
22	37	61.7	160	4 Q9RA58	Q9RA58 homo sapien
23	37	61.7	248	5 Q9BI08	Q9BI08 cooperia pu
24	37	61.7	248	5 Q9BI06	Q9BI06 cooperia pu
25	37	61.7	276	16 Q9JVF4	Q9JVF4 neisseria m
26	37	61.7	320	16 Q9R8S7	Q9R8S7 delinococcus
27	37	61.7	330	4 Q9BVX8	Q9BVX8 homo sapien
28	37	61.7	357	2 Q52865	Q52865 rhizobium 1
29	37	61.7	413	16 Q9PEW6	Q9PEW6 xylella fas
30	37	61.7	437	10 Q9FJ94	Q9FJ94 arabidopsis
31	37	61.7	443	10 Q9FNF1	Q9FNF1 arabidopsis
32	37	61.7	491	5 Q9BI04	Q9BI04 cooperia pu
33	37	61.7	511	2 Q06460	Q06460 thermus the
34	37	61.7	531	2 Q86716	Q86716 streptomyce
35	37	61.7	566	3 Q9HDT2	Q9HDT2 ustiliago ma
36	37	61.7	637	4 Q9BUP2	Q9BUP2 homo sapien
37	37	61.7	761	11 Q9Q209	Q9Q209 mus musculu
38	37	61.7	762	4 Q9UMS5	Q9UMS5 mus musculu
39	37	61.7	815	4 Q43273	Q43273 homo sapien
40	37	61.7	841	16 Q9ZJF0	Q9ZJF0 heliobacte
41	37	61.7	844	16 Q26014	Q26014 heliobacte
42	37	61.7	885	5 Q96230	Q96230 plasmodium
43	37	61.7	980	4 Q9NS55	Q9NS55 homo sapien
44	37	61.7	1033	11 Q920L3	Q920L3 mus musculu
45	37	61.7	1045	4 Q9NS56	Q9NS56 homo sapien

ALIGNMENTS

RESULT	ID	Q96SBO	PRELIMINARY:	PRT:	108 AA.
1	Q96SBO	01-DEC-2001 (TREMBLrel. 19, Created)			
DC	Q96SBO	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DE	ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN				
DE	VARIABLE REGION (FRAGMENT).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RX	SEQUENCE FROM N.A.				
RA	MEDLINE=98375893; PubMed=9712075;				
RA	Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;				
RT	"Molecular analysis of polyclonal monoclonal antibodies from				
RT	rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin				
RT	antibody V region genes."				
RL	J. Immunol. 161:2020-2031(1998).				
DR	EMBL, U96394; AAB68783.1; -.				
FT	NON_TER				
FT	SEQUENCE	108 AA;	11594 MM;	FAB5DC478A043F48	CRC64;

Query Match: 73.3%; Score 44; DB 4; Length 108;
Best Local Similarity: 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAMDSTLSG 9
| | | | |
DB 90 AAMDRLSG 98

RESULT 2
Q64697 PRELIMINARY: PRT: 197 AA.
AC Q64697;

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DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE (C POLYPEPTIDE ASSOCIATED
DE PROTEIN) (CD45-ASSOCIATED PROTEIN) (CD45-AP) (LSM) (SIMILAR TO PROTEIN
DE TYROSINE PHOSPHATASE, RECEPTOR TYPE, C-ASSOCIATED PROTEIN).
GN PTPCAP OR CD45-AP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=LYMPHOID;
RX MEDLINE=95046370; PubMed=7957956;
RA Shimizu Y., Ogawa H., Oka Y., Mizuno R., Sakoda S., Kishimoto T.,
RA Sugiyama H.;
RT "Isolation of a cDNA clone encoding a novel membrane protein expressed
RT in lymphocytes.";
RL FEBS Lett. 355:30-34(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=BL00D;
RX MEDLINE=94131987; PubMed=8300558;
RA Takeda A., Maizel A.L., Kitamura K., Ohta T., Kimura S.;
RT "Molecular cloning of the CD45-associated 30-kDa protein.";
RL J. Biol. Chem. 269:2357-2360(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON, NORMAL. 5 MONTH OLD MALE MOUSE.;
RA Strausberg R.;
RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: D10105; BAA00986.1; -.
DR EMBL: U03856; AAG7166.1; ALT_INIT.
DR EMBL: BC013273; AH13273.1; -.
DR MGD: MGI:97811; Ptpcap.
KW Receptor.
FT CONFLICT 55 55 R -> C (IN REF. 2).
FT SEQUENCE 197 AA; 20370 MW; B313F88693F084AA CRC64;
SQ

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Query Match 66.7%; Score 40; DB 11; Length 197;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 AAMDLSLG 9
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DB 178 AAMDLSAG 186

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RESULT 3
ID 09A925 PRELIMINARY; PRT; 355 AA.
AC 09A925;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN C1169.
DE C1169.
GN Caulobacter crescentus.
OS Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

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RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL: AE005795; AAK23153.1; -.
DR TIGR: CC1169; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 355 AA; 38552 MW; 3C4AEFA2825E5567 CRC64;

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OY 1 AAMDLS 8
| | | | |
DB 138 SAMDLS 145

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RESULT 4
ID 048629 PRELIMINARY; PRT; 133 AA.
AC 048629;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PUTATIVE AUXIN-REPPRESSED PROTEIN.
OS Prunus americana (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloidae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERGERON; TISSUE=MESOCARP PLUS EXOCARP;
RA Mbague A., Mbague D., Gomez R.-M., Fils-Lycaon B.;
RT "Molecular cloning and nucleotide sequence of a putative auxin-
RT repressed protein from apricot";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U93773; AAB8876.1; -.
SQ SEQUENCE 133 AA; 13696 MW; 0586EAE2CF6F4B CRC64;

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Query Match 65.0%; Score 39; DB 10; Length 133;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 3 WDDSLSGP 10
| | | | |
DB 8 WDDIVAGP 15

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RESULT 5
ID 09C7J7 PRELIMINARY; PRT; 140 AA.
AC 09C7J7;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE HYPOTHETICAL 14.8 KDA PROTEIN.
DE F14G9.17.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:49 ; Search time 84.18 Seconds

(without alignments)
3.192 Million cell updates/sec

Title: US-09-780-035-29_COPY_90_100
Perfect score: 60
Sequence: 1 AAMDSLSPGV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	95.0	111	4	US-08-983-607-27 Sequence 27, Appl
2	52	86.7	111	2	US-08-350-260A-441 Sequence 441, App
3	51	85.0	113	1	US-08-211-202-114 Sequence 114, App
4	49	81.7	9	2	US-08-665-202-60 Sequence 60, Appl
5	49	81.7	10	2	US-08-350-260A-339 Sequence 339, App
6	49	81.7	11	2	US-08-665-202-6 Sequence 6, Appl
7	49	81.7	98	1	US-08-211-202-111 Sequence 111, App
8	49	81.7	98	2	US-08-665-202-38 Sequence 38, Appl
9	49	81.7	109	4	US-09-240-274-59 Sequence 59, Appl
10	49	81.7	111	2	US-08-665-202-36 Sequence 36, Appl
11	49	81.7	111	2	US-08-665-202-43 Sequence 43, Appl
12	49	81.7	112	2	US-08-665-202-39 Sequence 39, Appl
13	49	81.7	113	1	US-08-211-202-112 Sequence 112, App
14	49	81.7	113	1	US-08-211-202-113 Sequence 113, App
15	49	81.7	258	2	US-08-665-202-5 Sequence 5, Appl
16	49	81.7	282	4	US-09-420-592A-7 Sequence 7, Appl
17	47	78.3	11	1	US-08-264-093-20 Sequence 20, Appl
18	47	78.3	109	4	US-09-240-274-55 Sequence 55, Appl
19	47	78.3	111	1	US-08-264-093-6 Sequence 6, Appl
20	47	78.3	112	4	US-09-023-769B-18 Sequence 18, Appl
21	46	76.7	111	2	US-08-350-260A-434 Sequence 434, App
22	46	76.7	111	2	US-08-665-202-40 Sequence 40, Appl
23	46	76.7	111	2	US-08-665-202-42 Sequence 42, App
24	45	75.0	11	2	US-08-350-260A-429 Sequence 429, App
25	45	75.0	11	2	US-08-350-260A-454 Sequence 454, App
26	45	75.0	109	4	US-09-240-274-56 Sequence 56, Appl
27	45	75.0	110	4	US-09-240-274-60 Sequence 60, Appl

28	44	73.3	11	2	US-08-350-260A-374	Sequence 374, App
29	44	73.3	109	4	US-09-240-274-57	Sequence 57, Appl
30	44	73.3	109	4	US-09-240-274-61	Sequence 61, Appl
31	43	71.7	10	2	US-08-350-260A-497	Sequence 497, App
32	43	71.7	11	2	US-08-665-202-104	Sequence 104, App
33	43	71.7	104	2	US-08-273-146-63	Sequence 63, Appl
34	43	71.7	111	2	US-08-652-816A-15	Sequence 15, Appl
35	42	70.0	11	2	US-08-665-202-8	Sequence 8, Appl
36	42	70.0	235	4	US-09-049-672A-12	Sequence 12, Appl
37	41	68.3	11	2	US-08-665-202-101	Sequence 101, App
38	41	68.3	111	2	US-08-665-202-41	Sequence 41, Appl
39	41	68.3	111	2	US-08-983-607-23	Sequence 23, Appl
40	40	66.7	10	2	US-08-350-260A-361	Sequence 361, App
41	40	66.7	10	2	US-08-350-260A-446	Sequence 446, App
42	40	66.7	10	2	US-08-350-260A-514	Sequence 514, App
43	40	66.7	11	2	US-08-350-260A-346	Sequence 346, App
44	40	66.7	11	2	US-08-350-260A-439	Sequence 439, App
45	40	66.7	11	2	US-08-350-260A-443	Sequence 443, App

ALIGNMENTS

RESULT 1
US-08-983-607-27
Sequence 27, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Department of Molecular Biophysics
and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 MB diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes

IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: 278
FEATURE:
NAME/KEY: light chain
US-08-983-607-27

Query Match 95.0%; Score 57; DB 4; Length 111;
Best Local Similarity 90.9%; Pred. No. 0.0041;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLSPV 11
Db 90 AAWDSLSPV 100

RESULT 2
US-08-350-260A-441
Sequence 441, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Missin, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W

REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-441

Query Match 86.7%; Score 52; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAWDSLSPV 11
Db 1 AAWDSLSPV 11

RESULT 3
US-08-211-202-114
Sequence 114, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOGGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
STREET: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-114

Query Match 85.0%; Score 51; DB 1; Length 113;
Best Local Similarity 90.9%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAMDLSLSPV 11
DB 90 AAMDLSLGRV 100

RESULT 4
US-08-665-202-60
Sequence 60, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-60

Query Match 81.7%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSLSC 9

DB 1 AAMDLSLSC 9

RESULT 5
US-08-350-260A-339
Sequence 339, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-339

Query Match 81.7%; Score 49; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSG 9
|||||

DB 1 AAWDDSLSG 9

RESULT 6

US-08-665-202-6
Sequence 6, Application US/08665202

Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.

TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202

FILING DATE: 13-JUN-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238

FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250

FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498

REFERENCE/DOCKET NUMBER: 02307E-061410

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-665-202-6

QY 1 AAWDDSLSG 9
|||||

DB 1 AAWDDSLSG 9

RESULT 7

US-08-211-202-111
Sequence 111, Application US/08211202

Patent No. 5565332

GENERAL INFORMATION:

APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Mattheus

APPLICANT: BAIER, Michael

APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach

NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:

ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/211,202

FILING DATE: 23-SEP-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9120252.3

FILING DATE: 23-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9120377.8

FILING DATE: 25-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206372.6

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: David W. Clough

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 28111/31960

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

INFORMATION FOR SEQ ID NO: 111:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-211-202-111

QY 1 AAWDDSLSG 9
|||||

DB 90 AAWDDSLSG 98

RESULT 8

US-08-665-202-38
Sequence 38, Application US/08665202

Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.

TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to

TITLE OF INVENTION: Tumor Antigens

NUMBER OF SEQUENCES: 141

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-38

Query Match 81.7%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSLG 9
Db 90 AAMDLSLG 98

RESULT 9
US-09-240-274-59
Sequence 59, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09566-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain M02
US-09-240-274-59

Query Match 81.7%; Score 49; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSLG 9
Db 89 AAMDLSLG 97

RESULT 10
US-08-665-202-36
Sequence 36, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-36

Query Match 81.7%; Score 49; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSLG 9
Db 90 AAMDLSLG 98

RESULT 11
US-08-665-202-43
Sequence 43, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:

APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-43

Query Match 81.7%; Score 49; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSIG 9
|||||
DB 90 AAMDLSIG 98

RESULT 12
US-08-665-202-39
Sequence 39, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-39

Query Match 81.7%; Score 49; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSIG 9
|||||
DB 90 AAMDLSIG 98

RESULT 13
US-08-211-202-112
Sequence 112, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Mattheus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-112

Query Match 81.7%; Score 49; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAWDSLGS 9
|||||
DB 90 AAWDSLGS 98

RESULT 14
US-08-211-202-113
Sequence 113, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAIER, Michel
APPLICANT: JESPER, Laurent Stephane Anne Therese
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-113

Query Match 81.7%; Score 49; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAWDSLGS 9
|||||
DB 90 AAWDSLGS 98

RESULT 15
US-08-665-202-5
Sequence 5, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: NO. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

;
; LENGTH: 258 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-665-202-5

Query Match 81.7%; Score 49; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSLG 9
Db 234 AAMDLSLG 242

Search completed: June 21, 2002, 09:21:49
Job time: 412 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:15:27 ; Search time 109.39 Seconds

(without alignments)
99.260 Million cell updates/sec

Title: US-09-780-035-18

Perfect score: 598

Sequence: 1 QVQLVQSGAEVKKPGASMKV.....YYCAKRGAGMGQGLVTVSS 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463.5	77.5	135	2 S49530	anti-Sm antibody V
2	461.5	77.2	118	2 S36265	Ig heavy chain V r
3	450	75.3	123	2 D33548	Ig heavy chain V-1
4	442	73.9	129	2 S46393	Ig heavy chain V r
5	442	73.9	142	2 A32483	Ig heavy chain V r
6	433.5	72.5	136	2 S31600	Ig heavy chain V r
7	430.5	72.0	132	2 S31596	Ig heavy chain V r
8	430.5	72.0	171	2 S23623	Ig heavy chain V r
9	428	71.6	104	2 S69899	Ig heavy chain V r
10	427	71.4	126	2 I44151	Ig heavy chain V r
11	422	70.6	98	2 S26938	Ig heavy chain V r
12	422	70.6	117	1 HVH035	Ig heavy chain pre
13	422	70.6	117	2 S18551	Ig heavy chain V r
14	419	70.1	109	2 PH1668	Ig heavy chain V r
15	417.5	69.8	110	2 PH1669	Ig heavy chain V r
16	415	69.4	117	2 S31680	Ig heavy chain V r
17	415	69.4	121	2 S20783	Ig heavy chain V r
18	414.5	69.3	120	2 S31999	Ig heavy chain V r
19	414	69.2	98	2 S26912	Ig heavy chain V r
20	411	68.7	127	2 S34014	Ig heavy chain V r
21	409.5	68.5	137	2 C41287	Ig heavy chain V r
22	405	67.7	122	2 S36271	Ig heavy chain pre
23	403.5	67.5	116	2 PH0959	Ig heavy chain V r
24	402.5	67.3	120	2 PH0962	Ig heavy chain V r
25	402	67.2	98	2 PH0871	Ig heavy chain V r
26	401.5	67.1	143	2 S26920	Ig heavy chain V r
27	401.5	67.0	120	2 S26789	Ig heavy chain pre
28	400.5	67.0	120	2 S26789	Ig heavy chain V r
29	400	66.9	125	2 PH0957	Ig heavy chain V r

30	399	66.7	160	2 PI0105	anti-PR2 erythrocy
31	397.5	66.5	110	2 PH1670	Ig heavy chain V r
32	397	66.4	117	1 HVH036	Ig heavy chain pre
33	396	66.2	98	2 S26910	Ig heavy chain V r
34	396	66.2	119	2 PH0961	Ig heavy chain V r
35	395.5	66.1	104	2 PH1665	Ig heavy chain V r
36	395.5	66.1	124	2 S19665	Ig heavy chain V r
37	395	66.1	129	2 A33548	Ig heavy chain V-1
38	394.5	66.0	122	2 PH0958	Ig heavy chain V r
39	394	65.9	98	2 S26918	Ig heavy chain V r
40	393	65.7	129	2 S36260	Ig heavy chain V r
41	392.5	65.6	128	2 PH0952	Ig heavy chain V r
42	392	65.6	125	2 S68170	Ig heavy chain V r
43	392	65.6	133	2 C33548	Ig heavy chain V r
44	392	65.6	627	2 S14683	Ig heavy chain V-1
45	391.5	65.5	132	2 PH0954	Ig mu chain precu
					Ig heavy chain V r

ALIGNMENTS

RESULT 1
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Mamoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <MAH>
A:Cross-references: EMBL:Z46348; NID:9560839; PIDN:CAA86467.1; PID:9560840
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
F:34-117/Domain: Immunoglobulin homology <IMM>

Query Match 77.5%; Score 463.5; DB 2; Length 135;
Best Local Similarity 75.0%; Pred. No. 3.7e-38;
Matches 87; Conservative 11; Mismatches 15; Indels 3; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASMKVSCKTSGYFTGYIHWRQAHGQGEWIGRLNPTGDANF 60
DB 20 QVQLVQSGAEVKKPGASVKSCAKSGYFTGYHWRQAHGQGEWIGRLNPTGDANF 79
QY 61 AEKFGGRALTRDTSISAVYQLDLSKSDPTAVYYCAKGE---GAWGQGLVTVSS 113
DB 80 AOKFGGRVTRDTSISAVYQLDLSKSDPTAVYYCARARTGYNYWGQGLVTVSS 135

RESULT 2
S36265
Ig heavy chain V region (clone alpha-MC1-1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, A.; Title: Human anti-self antibodies with high specificity from phage display libraries
A:Reference number: S36265; MUID:93178448
A:Accession: S36265
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GR1>
A:Cross-references: EMBL:Z18846; NID:933121; PIDN:CAA9298.1; PID:9339900
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IMM>

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:53 ; Search time 52.75 Seconds

(without alignments)
82.944 Million cell updates/sec

Title: US-09-780-035-18
Perfect score: 598

Scoring table: BLOSUM62

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	422	70.6	117	1	HV1G_HUMAN	P23083 homo sapien
2	401.5	67.1	147	1	HV1G_HUMAN	P01744 homo sapien
3	397	66.4	117	1	HV1B_HUMAN	P01743 homo sapien
4	365	61.0	117	1	HV13_MOUSE	P01757 mus musculus
5	365	61.0	138	1	HV48_MOUSE	P03980 mus musculus
6	363	60.7	117	1	HV12_MOUSE	P01756 mus musculus
7	360.5	60.3	139	1	HV07_MOUSE	P01751 mus musculus
8	357.5	59.8	117	1	HV51_MOUSE	P01751 mus musculus
9	356	59.5	118	1	HV1A_HUMAN	P06330 mus musculus
10	350.5	58.6	120	1	HV50_MOUSE	P01742 homo sapien
11	346.5	57.9	137	1	HV50_MOUSE	P06329 mus musculus
12	345	57.7	137	1	HV11_MOUSE	P01755 mus musculus
13	344	57.5	140	1	HV06_MOUSE	P01750 mus musculus
14	339	56.7	117	1	HV02_MOUSE	P01746 mus musculus
15	338	56.5	117	1	HV09_MOUSE	P01746 mus musculus
16	337	56.4	120	1	HV04_MOUSE	P01748 mus musculus
17	329.5	55.1	114	1	HV03_MOUSE	P01747 mus musculus
18	327	54.7	121	1	HV00_MOUSE	P01745 mus musculus
19	323.5	54.1	120	1	HV01_MOUSE	P01745 mus musculus
20	319	53.3	117	1	HV1E_HUMAN	P80421 homo sapien
21	318	53.2	125	1	HV10_MOUSE	P01754 mus musculus
22	316	52.8	117	1	HV1E_HUMAN	P06326 homo sapien
23	315	52.7	117	1	HV14_MOUSE	P01758 mus musculus
24	312	52.2	136	1	HV49_MOUSE	P06328 mus musculus
25	310	51.8	117	1	HV15_MOUSE	P01759 mus musculus
26	309	51.7	119	1	HV52_MOUSE	P06327 mus musculus
27	308	51.5	117	1	HV31_HUMAN	P01770 homo sapien
28	303.5	50.8	122	1	HV05_MOUSE	P01749 mus musculus
29	303.5	50.8	124	1	HV03_HUMAN	P01768 homo sapien
30	302.5	50.6	119	1	HV1E_HUMAN	P01761 homo sapien
31	300.5	50.3	119	1	HV37_MOUSE	P01607 mus musculus
32	296.5	49.6	124	1	HV40_MOUSE	P01840 mus musculus
33	294.5	49.2	126	1	HV1D_HUMAN	P01760 homo sapien
					HV3K_HUMAN	P01772 homo sapien

ALIGNMENTS

45	283.5	47.4	122	1	HV3A_HUMAN
44	284.5	47.6	121	1	HV3B_HUMAN
43	285	47.7	121	1	HV3J_HUMAN
42	285	47.7	119	1	HV3L_HUMAN
41	285.5	47.7	122	1	HV3H_HUMAN
40	286	47.8	113	1	HV3O_MOUSE
39	287.5	48.1	120	1	HV3U_HUMAN
38	288	48.2	115	1	HV3Z_MOUSE
37	288.5	48.2	114	1	HV01_CANRA
36	289	48.3	142	1	HV01_RAT
35	291	48.7	117	1	HV03_CARVU
34	293.5	49.1	119	1	HV38_MOUSE
33	295	49.7	117	1	P01808_mus musculus
32	296	49.7	117	1	P19180_carassus a
31	296.5	49.7	117	1	P01805_rattus norv
30	297	49.7	117	1	P01784_canis fami
29	297.5	49.7	117	1	P01801_mus musculus
28	298	49.7	117	1	P01782_homo sapien
27	298.5	49.7	117	1	P01799_mus musculus
26	299	49.7	117	1	P01773_homo sapien
25	299.5	49.7	117	1	P01773_homo sapien
24	300	49.7	117	1	P01771_homo sapien
23	300.5	49.7	117	1	P01753_homo sapien
22	301	49.7	117	1	P01762_homo sapien

[illegible]

HVIC_HUMAN STANDARD; PRT; 147 AA.
 ID HVIC_HUMAN
 AC P01744;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig heavy chain V-I region ND precursor (Fragments).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83065234; PubMed=6815656;
 RA Kenten J.H., Moigard H.V., Houghton M., Derbyshire R.B., Viney J.,
 RA Bell L.O., Gould H.J.,
 RT "Cloning and sequence determination of the gene for the human
 RT immunoglobulin epsilon chain expressed in a myeloma cell line."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
 RN [2]
 RP SEQUENCE OF 20-147.
 RA Benrich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
 RL (in) Bach M.K. (eds.);
 RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
 RL Marcel Dekker, New York (1978).
 CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN.
 DR PIR: A02026; EIHUND.
 DR HSSP; P01789; IMCP.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
 FT MOD_RES 20 20 PYROLIDONE CARBOXYLIC ACID.
 FT DISULFID 41 115 T -> V (IN REF. 2).
 FT CONFLICT 21 21 IH -> HI (IN REF. 2).
 FT CONFLICT 53 54 VG -> GV (IN REF. 2).
 FT CONFLICT 67 68 MISSING (IN REF. 2).
 FT NON_TER 125 125
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 16491 MW; 9489F72A5366C20 CRC64;

Query Match 67.1%; Score 401.5; DB 1; Length 147;
 Best Local Similarity 58.6%; Pred. No. 1,7e-36;
 Matches 75; Conservative 15; Mismatches 23; Indels 15; Gaps 1;

QY 1 QVQLVSGAEVKKPKGASKVSCSTGYTFGYTHWVROAHQGFEMIGRLNPTTGDA NF 60
 DB 20 QVQLVSGAEVKKPKGASVRSCKASGYTFIDSYTHWIRQAGHLEWVGWNPNSGGSY 79
 QY 61 AEKFGRAVALTRDTSISTAYLQDLSLKSDPTAVVYCA KE-----GAMGQ 105
 DB 80 APROGRTVTRDASFSRATVMDLSRSDSAVFYCAKSPFMSDYINPDYSTLDVWGQ 139
 QY 106 GTLVTVSS 113
 DB 140 GTLVTVSS 147

RESULT 3
 ID HVIB_HUMAN STANDARD; PRT; 117 AA.
 AC P01743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-I region HG3 precursor.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83144028; PubMed=6298778;
 RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
 RT "Evolutionary aspects of immunoglobulin heavy chain variable region
 RT (VH) gene subgroups.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib.ch).
 CC -----
 CC DR EMBL; J00240; AAA52988.1; -.
 DR PIR: A02024; HVHUG.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 66.4%; Score 397; DB 1; Length 117;
 Best Local Similarity 73.2%; Pred. No. 4,1e-36;
 Matches 71; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVKKPKGASKVSCSTGYTFGYTHWVROAHQGFEMIGRLNPTTGDA NF 60
 DB 20 QVQLVSGAEVKKPKGASVRSCKASGYTFNSYTHWVRQAPQGLEWMIINPNSGGSY 79
 QY 61 AEKFGRAVALTRDTSISTAYLQDLSLKSDPTAVVYCA 97
 DB 80 APROGRTVTRDTSISTAYLQDLSLKSDPTAVVYCA 116

RESULT 4
 ID HV13_MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region J558.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain V-region gene segments.";
 RL Nature 283:35-40(1980)
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS. MANY OF
 CC WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 DR PIR: A26242; MHMS5.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KM Immunoglobulin V region.

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:22 ; Search time 194.32 Seconds

(Without alignments)
100.599 Million cell updates/sec

Title:
US-09-780-035-18

Perfect score:
598

Sequence:
1 QVQVYSGAEVKKRPGASMKV.....YVAGKRGAMGCTIVTSS 113

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP rivirus: *
16: SP bacteriophage: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	452	75.6	125	4 Q9UL95	Q9UL95 homo sapien
2	446	74.6	119	4 Q9UL94	Q9UL94 homo sapien
3	430.5	72.0	124	4 Q9UL92	Q9UL92 homo sapien
4	413.5	69.1	159	4 Q960S0	Q960S0 homo sapien
5	394	65.9	614	4 Q96GAG	Q96GAG homo sapien
6	391	65.4	157	4 Q95978	Q95978 homo sapien
7	389	65.1	119	4 Q9GYZ2	Q9GYZ2 schistosoma
8	386.5	64.6	116	4 Q9UL89	Q9UL89 homo sapien
9	384	64.2	150	4 Q9Y298	Q9Y298 homo sapien
10	379	63.4	473	11 Q9DBL4	Q9DBL4 mus musculu
11	377	63.0	142	11 Q924Q1	Q924Q1 mus musculu
12	376.5	63.0	500	4 Q9BRV0	Q9BRV0 homo sapien
13	374.5	62.6	139	11 Q924R5	Q924R5 mus musculu
14	373.5	62.5	145	11 Q924P7	Q924P7 mus musculu
15	372.5	62.3	145	11 Q924R1	Q924R1 mus musculu
16	368	61.3	117	11 Q9QXE9	Q9QXE9 mus musculu

17	367	61.4	117	11 Q9QXE0	Q9QXE0 mus musculu
18	366.5	61.3	278	11 Q921K1	Q921K1 mus musculu
19	364.5	61.0	137	11 Q924R6	Q924R6 mus musculu
20	364.5	61.0	143	11 Q924R7	Q924R7 mus musculu
21	364.5	61.0	143	11 Q924R9	Q924R9 mus musculu
22	364.5	61.0	145	11 Q924R4	Q924R4 mus musculu
23	363.5	60.8	141	11 Q924Q4	Q924Q4 mus musculu
24	363	60.7	140	11 Q924R2	Q924R2 mus musculu
25	362.5	60.6	143	11 Q924R0	Q924R0 mus musculu
26	361.5	60.5	145	11 Q924Q6	Q924Q6 mus musculu
27	360.5	60.3	145	11 Q924Q7	Q924Q7 mus musculu
28	360.5	60.3	145	11 Q924Q0	Q924Q0 mus musculu
29	360.5	60.3	146	11 Q924C4	Q924C4 mus musculu
30	360.5	60.3	148	11 Q91WR1	Q91WR1 mus musculu
31	360	60.2	144	11 Q924P5	Q924P5 mus musculu
32	360	60.2	146	11 Q924Q3	Q924Q3 mus musculu
33	359.5	60.1	143	11 Q91VA2	Q91VA2 mus musculu
34	359	60.0	140	11 Q924P8	Q924P8 mus musculu
35	359	60.0	140	11 Q924P8	Q924P8 mus musculu
36	358	59.9	146	11 Q91WT1	Q91WT1 mus musculu
37	357.5	59.8	143	11 Q924R8	Q924R8 mus musculu
38	357	59.7	120	11 Q91V67	Q91V67 mus musculu
39	357	59.7	142	11 Q920E8	Q920E8 mus musculu
40	356.5	59.6	145	11 Q924Q2	Q924Q2 mus musculu
41	355.5	59.4	143	11 Q924R3	Q924R3 mus musculu
42	353.5	59.1	143	11 Q924Q5	Q924Q5 mus musculu
43	353.5	59.1	241	11 Q924Q0	Q924Q0 mus musculu
44	350.5	58.6	143	11 Q921A6	Q921A6 mus musculu
45	350	58.5	146	11 Q924Q8	Q924Q8 mus musculu

ALIGNMENTS

RESULT 1
Q9UL95 PRELIMINARY; PRT; 125 AA.
ID Q9UL95;
AC Q9UL95;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035019; AAD56255.1; -.
DR HSSP: P01810; 2PBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
FT NON_TER 1 125
FT NON_TER 125 125
SQ SHOUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 75.6%; Score 452; DB 4; Length 125;
Best local Similarity 66.4%; Pred. No. 7.4e-42;
Matches 83; Conservative 16; Mismatches 14; Indels 12; Gaps 1;
QY 1 QVQVYSGAEVKKRPGASMKVSCYTFYTHVVRQAHGQGFEMIGRLNPTTGDAF 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLVDSGAEVKKRPGASVSKVSKASGYTFYTHVVRQAHGQGFEMIGRLNPTTGDAF 60

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:13:07 ; Search time 245.49 Seconds

(without alignments)
51.128 Million cell updates/sec

Title: US-09-780-035-18

Perfect score: 598
Sequence: 1 QVQLVSGAIVKPKFGASKMV.....YYCAGKRGANGGCTIVTSS 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
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16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	598	100.0	113	22	AA65308
2	588	98.3	113	22	AA65352
3	470	78.6	123	19	AAW9228
4	461.5	77.2	120	18	AAW27551
5	458	76.6	245	22	AA67619
6	441	73.7	115	21	AA62172
7	441	73.7	115	21	AA62172
8	440	73.6	146	18	AAW2841
9	435	72.7	249	18	AAW24061
10	429.5	71.8	120	15	AAW5127
11	428.5	71.7	120	22	AAU02535

12	427.5	71.5	238	20	AAV21880
13	427	71.4	115	21	AA612169
14	427	71.4	125	21	AAV71447
15	427	71.4	241	20	AAV21882
16	425.5	71.2	124	20	AAV50150
17	424	70.9	156	22	AA676059
18	423.5	70.8	126	25	AA65609
19	423	70.7	120	22	AA662747
20	422	70.6	117	16	AA66296
21	422	70.6	121	19	AA653584
22	422	70.6	140	13	AA627051
23	422	70.6	236	19	AA649690
24	421.5	70.5	118	15	AA65126
25	421.5	70.5	118	15	AA65126
26	421.5	70.5	122	22	AA680305
27	421.5	70.5	135	13	AA629017
28	421	70.4	115	20	AA64095
29	421	70.4	119	16	AA681331
30	420.5	70.3	116	18	AA622418
31	420.5	70.3	135	13	AA629016
32	419	70.1	652	19	AA648650
33	418.5	70.0	146	21	AA653510
34	418	69.9	119	13	AA624560
35	418	69.9	140	18	AA621847
36	418	69.9	242	20	AA621884
37	417.5	69.8	124	20	AA650148
38	417.5	69.8	251	22	AA670171
39	416.5	69.6	118	18	AA627528
40	416.5	69.6	148	21	AA656295
41	416	69.6	119	21	AA671241
42	416	69.6	470	21	AA60936
43	415.5	69.5	137	20	AA608708
44	414.5	69.3	118	21	AA671444
45	414.5	69.3	128	21	AA671449

ALIGNMENTS

RESULT	1
AA65308	
ID	AA65308 standard; protein: 113 AA.
AC	AA65308;
DT	30-NOV-2001 (first entry)
XX	
XX	Anti-IL-18 antibody 2E1 heavy chain sequence.
DE	
KW	IL-18; interleukin-18; human; antibody; antitumoric; cerebroprotective;
KW	neurotrophic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW	immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX	
OS	Homo sapiens.
XX	
PN	W0200158956-A2.
XX	
PD	16-AUG-2001.
XX	
PF	09-FEB-2001; 2001WO-US04170.
XX	
PR	10-FEB-2000; 2000US-0181608.
XX	
PA	(BADI) BASF AG.
PI	Gaynor T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI	Duncan AR, Brocklehurst SM, Manovich J, Shortrock CP, Thompson JE;
XX	Lennard SN;
XX	WPI; 2001-550020/61.
DR	N-PSDB; AA647511.
XX	
PT	Novel antibodies and compounds capable of binding to human

PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

XX Example 2; Page 37; 91pp; English.

CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain sequence.

XX Sequence 113 AA;

Query Match 100.0%; Score 598; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 1e-52; Mismatches 0; Indels 0; Gaps 0;
Matches 113; Conservative 0;

QY 1 QVQLVDSGAEVKKRPASMKVSKCTSGYTFGTGYIHVWRQAHGSGFEMIGRLNPTGDAHF 60
DB 1 qvqlvsgaeavkkrpasmkvscktsygtftgyihwvrqahgsgfewigrlnptgdaanf 60

QY 61 AEKFGGRVALTRPTSTISATVLDLSKSDPTAVYYCAKGEKAGOGTLTVYSS 113
DB 61 ae kifgrvaltrdtsistaylqldslksdptavyycaqkgeagwggltlvvss 113

RESULT 2

ID AAG65352 standard; Protein; 113 AA.

AC AAG65352;

DT 30-NOV-2001 (first entry)

DE Anti-IL-18 antibody 2E1 heavy chain.

XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
XX neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiac;
XX immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.

OS Homo sapiens.

PN WO200158956-A2.

PD 16-AUG-2001.

PF 09-FEB-2001; 2001WO-US04170.

PR 10-FEB-2000; 2000US-0181608.

PA (BADI) BASF AG.

PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfield J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;
PI Lennard SM;

WPI; 2001-550020/61.

DR N-PSDB; AAA47511.

PT Novel antibodies and compounds capable of binding to human

PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

XX Example 2; Page 86; 91pp; English.

CC The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 heavy
CC chain.

XX Sequence 113 AA;

Query Match 98.3%; Score 588; DB 22; Length 113;
Best Local Similarity 99.1%; Pred. No. 1e-51; Mismatches 1; Indels 0; Gaps 0;
Matches 112; Conservative 0;

QY 1 QVQLVDSGAEVKKRPASMKVSKCTSGYTFGTGYIHVWRQAHGSGFEMIGRLNPTGDAHF 60
DB 1 qvqlvsgaeavkkrpasmkvscktsygtftgyihwvrqahgsgfewigrlnptgdaanf 60

QY 61 AEKFGGRVALTRPTSTISATVLDLSKSDPTAVYYCAKGEKAGOGTLTVYSS 113
DB 61 ae kifgrvaltrdtsistaylqldslksdptavyycaqkgeagwggltlvvss 113

RESULT 3

ID AAW79228 standard; Protein; 123 AA.

AC AAW79228;

DT 21-DEC-1998 (first entry)

DE Heavy chain variable region of human Amu 5-3.

XX Monoclonal antibody; Mab; LO-CD2a; humanised antibody; chimeric;
XX T-cell; immune response; CD2 antigen; graft-versus-host disease;
XX human lymphocyte; transplant rejection; autoimmune disease; Amu 5-3.

OS Homo sapiens.

PN US5817311-A.

PD 06-OCT-1998.

PF 07-JUN-1995; 95US-0472281.

PR 07-JUN-1995; 95US-0472281.

PR 05-MAR-1993; 93US-0027008.

PR 09-SEP-1993; 93US-0119032.

PR 29-MAR-1995; 95US-0407009.

PA (UNIV) UNIV CATHOLIQUE LOUVAIN.

PI Bazin H, Latime D;

WPI; 1998-556337/47.

PT Inhibition of T-cell mediated immune response with anti-CD2

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:14:57 ; Search time 84.18 Seconds

(without alignments)
32.788 Million cell updates/sec

Title: US-09-780-035-18

Sequence: 1 QVQLVSGAEVKKPKGASMKV.....YYCAGKEGAWGQGLTVASS 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	78.6	123	1	US-08-477-877B-94
2	470	78.6	123	2	US-08-472-281A-94
3	470	78.6	123	2	US-08-477-989B-94
4	467	78.1	117	4	US-09-025-769B-22
5	461.5	77.2	120	4	US-09-025-769B-36
6	461.5	77.2	120	4	US-09-025-769B-59
7	427	71.4	125	4	US-09-199-149-3
8	425.5	71.2	128	1	US-08-202-047-22
9	425.5	71.2	128	2	US-08-964-690-22
10	425	71.1	129	2	US-08-561-521-45
11	425	71.1	129	4	US-08-525-539A-77
12	425	71.1	129	5	PCT-US95-01219-45
13	422	70.6	117	3	US-08-545-809A-90
14	422	70.6	140	1	US-07-946-421-28
15	421.5	70.5	118	1	US-08-491-845-14
16	421.5	70.5	135	1	US-08-137-117D-102
17	421.5	70.5	135	2	US-08-436-717-102
18	421.5	70.5	137	3	US-08-513-968-38
19	421	70.4	119	5	US-08-561-521-10
20	420.5	70.3	116	5	PCT-US95-01219-10
21	420.5	70.3	116	5	US-08-561-521-41
22	420.5	70.3	119	1	PCT-US95-01219-41
23	420	70.2	119	1	US-08-300-386A-65
24	420	70.2	119	5	US-08-931-645-65
25	420	70.2	119	5	PCT-US95-11235-65
26	418	69.9	140	3	US-08-836-561-63
27	416.5	69.6	135	1	US-08-137-117D-112

28	416.5	69.6	135	2	US-08-436-717-112	Sequence 112, App
29	415.5	69.5	135	1	US-08-137-117D-100	Sequence 100, App
30	415.5	69.5	135	2	US-08-436-717-100	Sequence 100, App
31	414.5	69.3	118	4	US-09-199-149-5	Sequence 5, App1
32	414.5	69.3	128	4	US-09-199-149-12	Sequence 12, App1
33	413	69.1	123	2	US-08-482-882-86	Sequence 86, App1
34	413	69.1	123	2	US-08-483-389-86	Sequence 86, App1
35	413	69.1	123	2	US-08-487-113D-86	Sequence 86, App1
36	413	69.1	123	2	US-08-473-503-86	Sequence 86, App1
37	413	69.1	123	2	US-08-483-932-86	Sequence 86, App1
38	413	69.1	123	2	US-08-720-420A-86	Sequence 86, App1
39	413	69.1	123	3	US-08-714-017-86	Sequence 86, App1
40	413	69.1	123	3	US-08-475-680-86	Sequence 86, App1
41	412	68.9	140	3	US-08-836-561-74	Sequence 86, App1
42	411	68.7	121	1	US-08-202-047-23	Sequence 74, App1
43	411	68.7	121	3	US-08-964-690-23	Sequence 23, App1
44	410	68.6	123	1	US-08-482-882-53	Sequence 53, App1
45	410	68.6	123	2	US-08-483-389-53	Sequence 53, App1

ALIGNMENTS

RESULT 1
US-08-477-877B-94
; Sequence 94, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cecchi, Byrne, Bain, Gillfillan,
; STREET: 6 Becker Farm Road
; City: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1704
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Human Amu 5-3 heavy chain variable region.
; US-08-477-877B-94

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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:23:40 ; Search time 109.39 Seconds

(without alignments)
95.747 Million cell updates/sec

Title: US-09-780-035-19

Sequence: 1 SSELTPDPAVSVALGQIVRI.....RDSGCIHVFGGCKIVTLG 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR-71:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525	90.8	109	2	Ig lambda chain V
2	519	89.8	108	2	Ig lambda chain V
3	513.5	88.8	110	2	Ig lambda chain V
4	509	88.1	127	2	Ig lambda chain pr
5	503	87.0	109	2	Ig lambda chain V
6	498	86.2	108	2	Ig lambda chain V
7	494	85.5	233	2	Ig lambda chain V
8	493	85.3	108	1	Ig lambda chain V
9	488.5	84.5	146	2	Ig lambda chain V
10	487.5	84.3	110	2	Ig lambda chain V
11	465	80.4	233	2	Ig lambda chain V
12	463	80.1	115	2	Ig lambda chain V
13	463	80.1	115	2	Ig lambda chain V
14	418.5	72.4	106	2	Ig lambda chain V
15	399	69.0	105	2	Ig lambda chain V
16	392	67.8	119	2	Ig lambda chain V
17	385	66.6	190	2	Ig lambda chain V
18	378.5	65.5	120	2	Ig lambda chain V
19	373	64.5	107	2	Ig lambda chain V
20	364	63.0	231	2	Ig lambda chain V
21	363	62.8	231	2	Ig lambda chain V
22	362	62.6	120	2	Ig lambda chain V
23	361	62.5	226	2	Ig lambda chain V
24	359.5	62.2	212	2	Ig lambda chain V
25	359	62.1	151	2	Ig lambda chain V
26	358	61.9	108	1	Ig lambda chain V
27	358	61.9	132	2	Ig lambda chain V
28	356	61.6	231	2	Ig lambda chain V
29	354	61.2	106	1	Ig lambda chain V

30	354	61.2	233	2	S25747	Ig lambda chain -
31	352	60.9	106	1	LAH0ML	Ig lambda chain V-
32	351	60.7	107	1	LAH0UL	Ig lambda chain V-
33	345.5	59.8	232	2	S25756	Ig lambda chain V-
34	343	59.3	106	1	LAH0X	Ig lambda chain V-
35	341	59.0	109	2	S68171	Ig lambda chain V-
36	339	58.7	111	2	S36274	Ig lambda chain V-
37	337.5	58.4	112	2	S51148	Ig lambda chain V-
38	336	58.1	128	2	S24319	Ig lambda chain V-
39	335	58.0	105	2	S44124	Ig lambda chain pr
40	332	57.4	235	2	S05270	Ig lambda chain V
41	331	57.3	111	2	S47009	Ig lambda chain pr
42	327	56.6	95	2	S36065	Ig lambda chain V1
43	327	56.6	106	1	LAH0KN	Ig lambda chain V1
44	327	56.6	111	1	L2H0MC	Ig lambda chain V-
45	327	56.6	114	2	S16440	Ig lambda chain -

ALIGNMENTS

RESULT 1
S19663
Ig lambda chain V region (clone alpha-BSA3) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19663
R:Marks: J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Wint J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V gene libraries displayed on A:Reference number: S19663; MUID:92085276
A:Accession: S19663
A:Molecule type: mRNA
A:Residues: 1-109 <MAR>
A:Cross-references: EMBL:X61640; NID:929492; PIR:CAA43821.1; PID:q1340166
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMW>

Query Match 90.8% Score 525; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 7.7e-39;
Matches 100; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 SSELTPDPAVSVALGQIVRIITCGDLSLRHFYPMYQKPGQAPVLYIGKNNRPSGIPDR 60
DB 1 SSELTPDPAVSVALGQIVRIITCGDLSRYSYASWYQKPGQAPVLYIGKNNRPSGIPDR 60
QY 61 FSGSSSGNTGSLITITGAQAEDEADYICGSRDSCGIVHVFSGGKIVTLG 109
DB 61 FSGSSSGNTGSLITITGAQAEDEADYICNSRDSGNIHVFGGKIVTLG 109

RESULT 2
S47184
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47184
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from pat submitted to the EMBL Data Library, June 1994
A:Reference number: S47181
A:Accession: S47184
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <MCIC>
A:Cross-references: EMBL:X79783; NID:9506426; PIR:CAA56179.1; PID:9506427
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMW>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:48:14 ; Search time 52.75 Seconds

(without alignments)
80.008 Million cell updates/sec

Title: US-09-780-035-19

Sequence: 1 SSELTPDPAVSVALGQTVRTI.....RDSGCIHVFGGTRKTVLIG 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	493	85.3	108	1	LV3A_HUMAN
2	358	61.9	108	1	LV3A_HUMAN
3	358	61.9	111	1	LV3B_HUMAN
4	354	61.2	106	1	LV4A_HUMAN
5	352	60.9	106	1	LV4E_HUMAN
6	351	60.7	107	1	LV4C_HUMAN
7	343	59.3	106	1	LV4B_HUMAN
8	327	56.6	106	1	LV4D_HUMAN
9	327	56.6	111	1	LV2E_HUMAN
10	324	56.1	111	1	LV7A_HUMAN
11	324	56.1	130	1	LV1G_HUMAN
12	322	55.7	111	1	LV1D_HUMAN
13	315	54.5	111	1	LV2H_HUMAN
14	314.5	54.4	112	1	LV2K_HUMAN
15	311.5	53.9	112	1	LV6A_HUMAN
16	306	52.9	111	1	LV1C_HUMAN
17	305	52.8	111	1	LV2C_HUMAN
18	303	52.4	109	1	LV2E_HUMAN
19	303	52.4	111	1	LV2G_HUMAN
20	300	51.9	109	1	LV2I_HUMAN
21	297	51.4	111	1	LV2I_HUMAN
22	297	51.4	111	1	LV2A_HUMAN
23	295	51.0	111	1	LV6C_HUMAN
24	292.5	50.6	110	1	LV2J_HUMAN
25	290	50.2	109	1	LV1F_HUMAN
26	288	49.8	111	1	LV2B_HUMAN
27	287	49.7	111	1	LV2D_HUMAN
28	285	49.3	111	1	LV1A_HUMAN
29	284	49.1	113	1	LV1L_HUMAN
30	283.5	49.0	112	1	LV1B_HUMAN
31	283.5	49.0	131	1	LV6E_HUMAN
32	280.5	48.5	112	1	LV6H_HUMAN
33	280	48.4	111	1	LV6D_HUMAN

34	271.5	47.0	110	1	KV13_RABIT	P01694 oryctolagus
35	262.5	45.4	112	1	LV6B_HUMAN	P01722 homo sapien
36	256.5	44.4	136	1	KV5B_MOUSE	P01634 mus musculu
37	256	44.3	117	1	KV10_RABIT	P01601 oryctolagus
38	252.5	43.7	108	1	KV1M_HUMAN	P01605 homo sapien
39	252.5	43.7	129	1	LV1B_MOUSE	P01724 mus musculu
40	250.5	43.3	110	1	KV01_RABIT	P01682 oryctolagus
41	246	42.6	133	1	KV4B_HUMAN	P06313 homo sapien
42	245.5	42.5	108	1	KV1P_HUMAN	P80362 homo sapien
43	244.5	42.3	108	1	KV1P_HUMAN	P01608 homo sapien
44	243.5	42.1	129	1	LV1D_MOUSE	P01726 mus musculu
45	242.5	42.0	108	1	KV07_RABIT	P01688 oryctolagus

ALIGNMENTS

RESULT 1	LV3A_HUMAN	STANDARD:	PRT: 108 AA.
ID	LV3A_HUMAN		
AC	P01714;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig lambda chain V-III region SH.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=70166723; PubMed=4909564;		
RA	Titani K., Wikler M., Shinoda T., Putnam F.W.;		
RT	"The amino acid sequence of a lambda type Bence-Jones protein. 3. The		
RT	complete amino acid sequence and the location of the disulfide		
RT	bridges.";		
RL	J. Biol. Chem. 245: 2171-2176 (1970).		
CC	-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.		
DR	PIR; A01980; L3HUSH.		
DR	HSSP; P01703; 7FAB.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig_1.		
DR	SMART; SM00406; IGV_1.		
KW	Immunoglobulin V region; Bence-Jones protein.		
FT	DISULFID 21 86		
FT	NON_TER 108 108		
SQ	SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;		

Query Match 85.3%; Score 493; DB 1; Length 108;
Best Local Similarity 87.0%; Pred. No. 4.5e-42;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY	2	SELTQDPAAVSVALGQTVRTICGDSLRHFPYMWQKQGAQVATYKNNRPSGIPRF	61
DB	1	SELTQDPAAVSVALGQTVRTICGDSLRGTDAAWYQKFGQAPLVTYKNNRPSGIPRF	60
QY	62	SSGSGNTGSLTTITGAQAEDEADYYCGSRDSSGCIHVFGGTRKTVLIG	109
DB	61	SSSGSGHTASLTITGAQAEDEADYYCNSRDSGKIVLFGGTRKTVLIG	108

RESULT 2	LV5A_HUMAN	STANDARD:	PRT: 108 AA.
ID	LV5A_HUMAN		
AC	P01719;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig lambda chain V-V region DEL.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=75112179; PubMed=4452363;
 RT Eulitz M.;
 RT "A new subgroup of human I-chains of the lambda-type. Primary
 structure of Bence-Jones protein DEL.";
 RL Eur. J. Biochem. 50:49-69(1974).
 CC -1- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA
 CC CHAIN SUBGROUP V.
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR HSP: A01985; LSHUDL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11342 MW; B8E8ED9C9C9E451 CRC64;
 Query Match 61.9%; Score 358; DB 1; Length 108;
 Best Local Similarity 65.1%; Pred. No. 9.3e-29;
 Matches 69; Conservative 13; Mismatches 24; Indels 0; Gaps 0;
 OY 4 LTODPVSVALGQTVRITCGDSLRFHYPNWYQOKPGQAPVLYTGKNNRPSGIPDRFSG 63
 DB 3 LTQPPSVAVAPGETARTLTGNDISESVHWYQOKPGQAPVLYTFDRDRSGIPIRPSG 62
 OY 64 SSGSNTGSLITTCGAQAEDEADYCGSRDSSGIIHVFGGSKTYVLG 109
 DB 63 SNGSTATLITISRVENAGDEADYCEWMDRAHYVFGGKTYVLG 108
 RESULT 3
 ID LV3B_HUMAN STANDARD; PRT; 111 AA.
 AC P06748;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Ig lambda chain V-III region LOI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE, SUBUNIT, DISEASE, AND 3D-STRUCTURE MODELLING.
 RC TISSUE-Ofine;
 RX MEDLINE=99441384; PubMed=10510403;
 RA Jocranta T.S., Solomon A., Pangburn M.K., Zipfel P.F., Meri S.;
 RT "Nephritogenic lambda light chain dimer: a unique human
 multiatom antibody against complement factor H.";
 RL J. Immunol. 163:4590-4596(1999).
 CC -1- FUNCTION: ACTIVATES THE ALTERNATIVE COMPLEMENT PATHWAY BY BINDING
 CC TO THE SHORT CONSENSUS REPEAT DOMAIN 3 (SCR3) OF FACTOR H.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- DISEASE: THE BLOCKING OF FACTOR H BY LOI PROTEIN LEADS TO THE
 CC DEVELOPMENTAL OF MEMBRANOPROLIFERATIVE GLOMERULONEPHRITIS (MPGN).
 DR PDB: 2LOI; 29-DEC-99.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KM Immunoglobulin V region; 3D-structure.
 FT BINDING 15 25 SCR3.
 FT BINDING 25 25 SCR3.
 FT BINDING 29 29 SCR3.
 FT BINDING 48 51 SCR3.
 FT BINDING 94 94 SCR3.
 FT BINDING 21 86 BY SIMILARITY.
 FT DISULFID

FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 11935 MW; 69498BEBDE82053 CRC64;
 Query Match 61.9%; Score 358; DB 1; Length 111;
 Best Local Similarity 66.7%; Pred. No. 9.5e-29;
 Matches 70; Conservative 12; Mismatches 23; Indels 0; Gaps 0;
 OY 4 LTODPVSVALGQTVRITCGDSLRFHYPNWYQOKPGQAPVLYTGKNNRPSGIPDRFSG 63
 DB 3 LTQPPSVAVAPGETARTLTGNDISESVHWYQOKPGQAPVLYTFDRDRSGIPIRPSG 62
 OY 64 SSGSNTGSLITTCGAQAEDEADYCGSRDSSGIIHVFGGSKTYVL 108
 DB 63 SNGSTATLITISRVENAGDEADYCCQAMDSSSHVYVFGGKTYVL 107
 RESULT 4
 ID LV4A_HUMAN STANDARD; PRT; 106 AA.
 AC P01715;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-IV region Bau.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=75059189; PubMed=4435717;
 RA Baczko K., Braun D., Hilschmann N.;
 RT "Pattern of antibody structure, the primary structure of monoclonal
 immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones
 protein Bau.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR PIR: A01981; LAHUBU.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KM Immunoglobulin V region; Bence-Jones protein.
 FT NON_TER 106 106
 SQ SEQUENCE 106 AA; 11305 MW; 4B6A688E0EC46571 CRC64;
 Query Match 61.2%; Score 354; DB 1; Length 106;
 Best Local Similarity 66.0%; Pred. No. 2.3e-28;
 Matches 70; Conservative 11; Mismatches 23; Indels 2; Gaps 1;
 OY 4 LTODPVSVALGQTVRITCGDSLRFHYPNWYQOKPGQAPVLYTGKNNRPSGIPDRFSG 63
 DB 3 LTQPPSVAVAPGETARTLTGNDISESVHWYQOKPGQAPVLYTFDRDRSGIPIRPSG 62
 OY 64 SSGSNTGSLITTCGAQAEDEADYCGSRDSSGIIHVFGGSKTYVLG 109
 DB 63 SNGSTATLITISRVENAGDEADYCCQAMDSSSHVYVFGGKTYVLG 106
 RESULT 5
 ID LV4E_HUMAN STANDARD; PRT; 106 AA.
 AC P06889;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig lambda chain V-IV region MOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 09:47:15 ; Search time 194.32 Seconds

(without alignments)
97.038 Million cell updates/sec

Title: US-09-780-035-19

Sequence: 1 SSETQDPVAVSVALGQTVRI.....RDSGJHVVFGGKTVTLG 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_protist:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	509	88.1	107	4 Q9NSD6	Q9NSD6 homo sapien
2	349.5	60.5	107	4 Q9UL82	Q9UL82 homo sapien
3	327.5	56.7	236	4 Q96E61	Q96E61 homo sapien
4	312	54.0	116	4 Q96JD0	Q96JD0 homo sapien
5	298.5	51.6	112	4 Q96JD1	Q96JD1 homo sapien
6	288	49.8	112	4 Q96JD2	Q96JD2 homo sapien
7	286	49.5	233	4 Q96I69	Q96I69 homo sapien
8	272	47.1	235	11 Q99M11	Q99M11 mus musculu
9	258	44.6	108	4 Q96S80	Q96S80 homo sapien
10	256	44.3	107	4 Q9UL81	Q9UL81 homo sapien
11	249	43.1	109	4 Q96SA9	Q96SA9 homo sapien
12	244.5	42.3	108	4 Q9UL78	Q9UL78 homo sapien
13	240	41.5	233	11 Q9UL77	Q9UL77 homo sapien
14	233.5	40.4	111	11 Q91V32	Q91V32 m adult mal
15	232.5	40.2	298	11 Q920E9	Q920E9 mus musculu
16					Q9GYF0 mus musculu

17	232	40.1	109	4 Q9UL85	Q9UL85 homo sapien
18	231.5	40.1	109	6 Q9N0W5	Q9N0W5 oryctolagus
19	228.5	39.5	211	11 Q91XL0	Q91XL0 mus musculu
20	227.5	39.4	109	11 Q920E6	Q920E6 mus musculu
21	227	39.3	109	4 Q9UL86	Q9UL86 homo sapien
22	226	39.1	101	11 Q9UL78	Q9UL78 mus musculu
23	224	38.8	109	11 Q9ET13	Q9ET13 mus musculu
24	223	38.6	97	11 Q9UL76	Q9UL76 mus musculu
25	223	38.6	106	5 Q9UL10	Q9UL10 schistosoma
26	223	38.6	238	11 Q99M37	Q99M37 mus musculu
27	220.5	38.1	107	11 Q9ER29	Q9ER29 mus musculu
28	220.5	38.1	108	4 Q9UL70	Q9UL70 homo sapien
29	219.5	38.0	104	11 Q9UL82	Q9UL82 mus musculu
30	218.5	37.8	214	11 Q9R1A5	Q9R1A5 mus musculu
31	217.5	37.6	108	4 Q9UL79	Q9UL79 homo sapien
32	216.5	37.5	114	4 Q9UL80	Q9UL80 homo sapien
33	215.5	37.3	108	4 Q9UL83	Q9UL83 homo sapien
34	215	37.2	103	11 Q9UL80	Q9UL80 mus musculu
35	212	36.7	99	11 Q9UL74	Q9UL74 mus musculu
36	210	36.3	235	11 Q91W12	Q91W12 mus musculu
37	208.5	36.1	233	11 Q91WS9	Q91WS9 mus musculu
38	199.5	34.5	116	4 Q96PF6	Q96PF6 homo sapien
39	199	34.4	241	11 Q921A6	Q921A6 mus musculu
40	198.5	34.3	154	11 Q91AK2	Q91AK2 mus musculu
41	190.5	33.0	234	11 Q91WF8	Q91WF8 mus musculu
42	186.5	32.3	127	11 Q925S9	Q925S9 mus musculu
43	183.5	31.7	107	11 Q9UL84	Q9UL84 mus musculu
44	179.5	31.1	135	4 Q9H5Z4	Q9H5Z4 homo sapien
45	170.5	29.5	93	4 Q9UL76	Q9UL76 homo sapien

ALIGNMENTS

RESULT	ID	Q9NSD6	PRELIMINARY;	PRT;	107 AA.
Q9NSD6	Q9NSD6	Q9NSD6			
DT	01-OCF-2000 (TREMBLrel. 15, Created)				
DT	01-OCF-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	HYPOTHEORETICAL PROTEIN (FRAGMENT).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
FN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIMPHOCYTE;				
RA	Hohmann A.;				
RT	"Autoimmunity."				
RL	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; I43092; AAA69746.2; -.				
DR	HSSP; P01709; ZMCG.				
DR	InterPro; IPR003006; IG_MHC.				
DR	InterPro; IPR003596; IG_V.				
DR	Pfam; PF00047; IG_1.				
DR	SMART; SM00406; IG_V.				
FT	NON_TER	1			
FT	NON_TER	107			
SO	SEQUENCE	107 AA;	11306 MW;	A2B04B37187A5F00 CRC64;	
Query Match	88.1%;	Score 509;	DB 4;	Length 107;	
Best Local Similarity	89.7%;	Pred. No. 5.9e-46;			
Matches	96;	Conservative	3;	Mismatches	8;
				Indels	0;
				Gaps	0;
QY	3 ELTDDPVAVALGQTVRIITCGDSLRFHYPNWYQKPGQAPVYITGKNNRPSGIDRRS 62				
Db	1 ELTDDPVAVALGQTVRIITCGDSLRFHYPNWYQKPGQAPVYITGKNNRPSGIDRRS 60				
QY	63 GSGSGNTGSLITGCAQAEADADYVCGSRDSSGIHVVFGGKTVTLG 109				

Db 61 GSSSGNTASLTITGAQAEADYCYCNSRDSGNHAFVGGTKLTVLG 107

RESULT 2

Q90L82 PRELIMINARY; PRT; 107 AA.

AC Q90L82;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE MOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION

OS (FRAGMENT).

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

fevus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035032; AAD56268.1; -.

DR HSSP; P01703; 7FAB.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig_1.

DR SMART; SM00406; IgV_1.

FT NON_TER 1

FT NON_TER 107

SQ SEQUENCE 107 AA; 11445 MW; 52FOCC1AB26821DC CRC64;

Query Match

Best Local Similarity 60.5%; Score 349.5; DB 4; Length 107;

Matches 71; Conservative 12; Mismatches 23; Indels 3; Gaps 2;

QY 1 SSETLPDPAVSVALGQVTRITCGDSLRFHPYPMWYQKPGQAPLVLYIGKNNRPSGIPDR 60

Db 1 SYELTPSSVSVPQGRTRITCSGDLAKKARFQKPGQAPLVLYIGKNNRPSGIPDR 60

QY 61 FSSGSGSGNTGSLTTGAQAEADYCYC-GSRDSSGSHVFGGTRKTVLG 108

Db 61 FSSGSGSGTTLTISGAQVEADYCYCSASDNG--RVFGGTRKTVLG 107

RESULT 3

Q96E61 PRELIMINARY; PRT; 236 AA.

AC Q96E61;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE UNKNOWN (PROTEIN FOR MGC:17259).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRIN. AND GLOBLASTOMA WITH EGFR AMPLIFICATION;

RA Strausberg R.;

RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC012876; AAH12876.1; -.

SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB362FED957 CRC64;

Query Match

Best Local Similarity 62.2%; Score 327.5; DB 4; Length 236;

Matches 69; Conservative 8; Mismatches 31; Indels 3; Gaps 1;

QY 2 SSETLPDPAVSVALGQVTRITCGDSLRFHPYPMWYQKPGQAPLVLYIGKNNRPSGIP 58

Db 21 SYLAQPPSVSGAPGQVTRITCSGSSNTGAGYAVHMYQAPPAKRVLYIGKNNRPSGVP 80

QY 59 DRPSGSGSGNTGSLTTGAQAEADYCYGSRDSSGSHVFGGTRKTVLG 109

Db 81 DRPSGSGSGTSLTITGAQAEADYCYGSDGSLGSGVFAGTRKTVLG 131

RESULT 4

Q96JD0 PRELIMINARY; PRT; 116 AA.

AC Q96JD0;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION SAR (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BONE MARROW;

RA Perleth V., Casarini S., Colla Vignarelli M., Merlini G.;

RL "Amyloid lambda 6 light chain variable region SAR."

DR EMBL; AF267875; AAK58587.1; -.

FT NON_TER 1

FT NON_TER 116

SQ SEQUENCE 116 AA; 12294 MW; F7B0E9F49FAE369E CRC64;

Query Match

Best Local Similarity 54.0%; Score 312; DB 4; Length 116;

Matches 65; Conservative 13; Mismatches 28; Indels 4; Gaps 2;

QY 4 LTQDPVAVSVALGQVTRITCGD-SLRHPYPMWYQKPGQAPLVLYIGKNNRPSGIPDR 61

Db 4 LTQDPVAVSVALGQVTRITCGD-SLRHPYPMWYQKPGQAPLVLYIGKNNRPSGIPDR 63

QY 62 SGS-SGSGNTGSLTTGAQAEADYCYGSRDSSGSHVFGGTRKTVLG 109

Db 64 SGSIDSSNSASLTISGLKTEADYCYGSDYSGVYIGVFGGTRKTVLG 113

RESULT 5

Q96JD1 PRELIMINARY; PRT; 112 AA.

AC Q96JD1;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION PIP (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BONE MARROW;

RA Perleth V., Casarini S., Colla Vignarelli M., Merlini G.;

RL "Amyloid lambda 6 light chain variable region PIP."

DR EMBL; AF267874; AAK58586.1; -.

FT NON_TER 1

FT NON_TER 112

SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

Query Match

Best Local Similarity 51.6%; Score 298.5; DB 4; Length 112;

Matches 61; Conservative 16; Mismatches 28; Indels 5; Gaps 3;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 09:20:13 ; Search time 245.49 Seconds

(without alignments)
49.318 Million cell updates/sec

Title: US-09-780-035-19

Perfect score: 1 SSSLRQDPANVSVALGQTVRI.....RDSGTHVVGEGGKVTVLG 109

Sequence:

Scoring table: BLOSUM62

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	100.0	109	22	AA65309
2	578	100.0	109	22	AA65353
3	525	90.8	109	22	AAU02513
4	525	90.8	229	19	AAW49694
5	525	90.8	236	19	AAW49690
6	525	90.8	237	19	AAW49691
7	525	90.8	239	19	AAW49692
8	525	90.8	254	19	AAW49693
9	525	90.8	280	22	AAE02186
10	525	90.8	282	22	AAE02185
11	525	90.8	309	20	AAW83322

12	525	90.8	312	20	AAW83323	Single chain Apo-2
13	522	90.3	109	18	AAW15525	Anti-TGF beta-2 sc
14	522	90.3	115	22	AA65559	Amino acid sequenc
15	521	90.1	108	22	AA62939	Amino acid sequenc
16	519	89.8	108	21	AA144616	Human antibody clo
17	519	89.8	249	18	AAW24061	Human MSX receptor
18	516	89.3	109	22	AAU02504	Anti-adipocyte mon
19	516	89.3	240	22	AA646052	Human TF anti-idlo
20	515	89.1	111	21	AAV95559	Human LH3 monocl
21	515	89.1	115	22	AA65557	Human acid sequenc
22	514	88.9	109	22	AAU02527	Anti-adipocyte mon
23	513	88.8	107	22	AA62969	Human TF anti-idlo
24	511	88.4	239	22	AA646054	Human TF anti-idlo
25	510.5	88.3	108	21	AAV95185	Anti-platelet glyc
26	510.5	88.3	108	21	AAV95185	Anti-platelet glyc
27	508	87.9	108	22	AA62937	Amino acid sequenc
28	506	87.5	106	22	AAU02531	Anti-adipocyte mon
29	504.5	87.3	107	21	AAV95194	Anti-platelet glyc
30	504.5	87.3	107	21	AAV95215	Anti-platelet glyc
31	504.5	87.3	237	21	AAV95219	Anti-platelet glyc
32	503.5	87.1	110	18	AAW15526	Anti-TGF beta-2 sc
33	501	86.7	108	22	AA62935	Amino acid sequenc
34	501	86.7	108	22	AA62945	Amino acid sequenc
35	501	86.7	108	22	AA62961	Amino acid sequenc
36	500.5	86.6	238	21	AAV95198	Anti-platelet glyc
37	500.5	86.6	242	21	AAV15127	Anti-murine CTLA-4
38	500	86.5	109	22	AAU02509	Anti-adipocyte mon
39	499	86.3	108	22	AA62933	Amino acid sequenc
40	499	86.3	109	22	AAU02511	Anti-adipocyte mon
41	499	86.3	236	22	AA646055	Human TF anti-idlo
42	498	86.2	108	22	AAU02632	Anti-adipocyte mon
43	498	86.2	109	18	AAW19884	CEA-specific antib
44	495	85.6	107	18	AAW15528	Anti-TGF beta-2 sc
45	494.5	85.6	109	18	AAW08583	Human antibody C4.

ALIGNMENTS

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RESULT 1
AA65309
ID   AA65309 standard; protein; 109 AA.
AC   AA65309;
DT   30-NOV-2001 (first entry)
DE   Anti-IL-18 antibody 2E1 light chain sequence.
KW   IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW   nootropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW   immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.
XX
XX   OS   Homo sapiens.
XX   PN   WO200158956-A2.
XX
XX   PD   16-AUG-2001.
XX
XX   PF   09-FEB-2001; 2001WO-US04170.
XX
XX   PR   10-FEB-2000; 2000US-0181608.
XX
XX   (BADI ) BASF AG.
XX
XX   Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J,
XX   Lennard SN, Duncann AR, Brocklehurst SM, Mankovich J, Shortrock CP, Thompson JR;
XX   WPI; 2001-550020/61.
XX   N-PSDB; AAH47512.
XX
XX   Novel antibodies and compounds capable of binding to human
XX

```

PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

PS Example 2; Page 38; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and schizophrenia). Treatment with an anti-IL-18
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain sequence.

XX Sequence 109 AA;

Query Match 100.0%; Score 578; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSELTDPAVSVALGQTVRTICGDSLRFHPYPMWYQKPGQAPVLYIGKNNRPSGIPDR 60
Db 1 sseltdpavsva1gqvrticgds1rfhpypmwyqkpgqapvlyigknnrpsgipdr 60

QY 61 FSGSSGNTGSLRTTGAQAEADYCYGSRDSSG1HVFEGGCTKVTYLG 109
Db 61 fsgsgntgslrttgaqaeadyycgsrdssg1hvfeggtkvtlvg 109

RESULT 2

AA65353 ID AAG65353 standard; protein; 109 AA.

AC AAG65353;

DT 30-NOV-2001 (first entry)

DE Anti-IL-18 antibody 2E1 light chain sequence.

XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW nootropic; neurological; antiinflammatory; antiparkinsonian; cardiac;
KM immunosuppressive; antidepressant; neuroleptic; hepatotropic; 2E1.

OS Homo sapiens.

PN WO200158956-A2.

PD 16-AUG-2001.

PF 09-FEB-2001; 2001WO-US04170.

PR 10-FEB-2000; 2000US-0181608.

PA (BADI) BASF AG.

PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfield J;
PI Duncan AR, Brocklehurst SM, Mankovich J, Shortrock CP, Thompson JE;
PI Lennard SN;

XX WPI: 2001-550020/61.

DR N-PSDB; AAAH47512.

PT Novel antibodies and compounds capable of binding to human

PT interleukin-18 useful for treating, e.g., inflammatory disorders,
PT neurological disorders, heart failure, myocardial infarction, and
PT autoimmune diseases -

PS Example 2; Page 88; 91pp; English.

XX The invention provides isolated antibodies, or antigen-binding portions,
CC that are capable of binding to human interleukin-18 (IL-18). The
CC antibodies may be used to inhibit human IL-18 activity in, and treat a
CC disorder where IL-18 is detrimental in, a human subject suffering from,
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,
CC inflammatory bowel disease, and osteoarthritis), neurological disorders
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and
CC stroke), heart failure, myocardial infarction, autoimmune diseases such
CC as autoimmune hepatitis and schizophrenia). Treatment with an anti-IL-18
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18
CC antibody may occur before, concurrent, or after administration of a
CC second agent selected from an antibody, or fragment, capable of binding
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory
CC agents. The present sequence represents an anti-IL-18 antibody 2E1 light
CC chain sequence.

XX Sequence 109 AA;

Query Match 100.0%; Score 578; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSELTDPAVSVALGQTVRTICGDSLRFHPYPMWYQKPGQAPVLYIGKNNRPSGIPDR 60
Db 1 sseltdpavsva1gqvrticgds1rfhpypmwyqkpgqapvlyigknnrpsgipdr 60

QY 61 FSGSSGNTGSLRTTGAQAEADYCYGSRDSSG1HVFEGGCTKVTYLG 109
Db 61 fsgsgntgslrttgaqaeadyycgsrdssg1hvfeggtkvtlvg 109

RESULT 3

AA002513 ID AA002513 standard; protein; 109 AA.

AC AA002513;

DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 7.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.

OS Homo sapiens.

PN WO200127279-A1.

PD 19-APR-2001.

PF 11-OCT-2000; 2000WO-GB03900.

PR 12-OCT-1999; 99US-0158812.

PA (CAMB-) CAMBRIDGE ANTIPODY TECHNOLOGY.

PI Edwards BM, Main SH, Vaughan TJ;

DR WPI: 2001-282031/29.

DR N-PSDB; AAS03413.

XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity
PT related diseases -
XX

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2002, 09:21:44 ; Search time 84.18 Seconds
(without alignments)
31.627 Million cell updates/sec

Title: US-09-780-035-19
Perfect score: 578
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	525	90.8	280	4	US-09-260-527-1
3	525	90.8	309	4	US-09-079-029-9
4	525	90.8	312	4	US-09-079-029-9
5	498	85.2	109	2	US-08-652-816A-16
6	494.5	85.6	109	2	US-08-652-816A-16
7	462.5	80.0	104	4	US-08-793-450-2
8	462.5	80.0	238	4	US-08-793-450-2
9	462	79.9	97	2	US-08-665-202-35
10	458	79.2	104	4	US-09-240-274-49
11	445	77.0	106	4	US-09-240-274-49
12	441	76.3	106	4	US-09-240-274-48
13	434	75.1	106	4	US-09-240-274-48
14	433	74.9	103	2	US-08-273-146-71
15	419.5	72.6	108	4	US-09-025-769B-20
16	414.5	71.7	105	1	US-08-488-113B-157
17	414.5	71.7	105	1	US-08-477-484B-157
18	414.5	71.7	105	1	US-08-107-669D-21
19	414.5	71.7	105	1	US-08-472-788A-21
20	414.5	71.7	105	2	US-08-477-531B-21
21	414.5	71.7	105	2	US-08-646-360-157
22	414.5	71.7	105	2	US-08-082-842A-21
23	414.5	71.7	105	2	US-08-839-765-157
24	414.5	71.7	105	4	US-09-136-389-157
25	402	69.6	108	1	US-08-360-125-12
26	402	69.6	108	2	US-08-450-578-12
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30	384	66.4	109	1	US-08-478-039-91	Sequence 91, Appl
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32	379	65.6	107	4	US-09-025-769B-55	Sequence 34, Appl
33	379	65.6	107	4	US-09-025-769B-55	Sequence 55, Appl
34	374.5	64.8	143	2	US-08-345-321-8	Sequence 8, Appl
35	374	64.7	108	1	US-08-259-372A-10	Sequence 10, Appl
36	374	64.7	108	1	US-08-468-671-10	Sequence 10, Appl
37	374	64.7	224	3	US-08-487-550-2	Sequence 2, Appl
38	350	60.6	109	4	US-09-202-181-2	Sequence 2, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 3, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 278
; TYPE: PRT
; ORGANISM: UNKNOWN
; FEATURE:
; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected
; OTHER INFORMATION: from a naive phage display library known as the
; OTHER INFORMATION: Synthetic scfv Library (#1) from the Centre for
; OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK
US-09-260-527-3

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QY 61 FSGSSGNTGSLITLITGAQAEDEADYYCGSRDSSGCIHVFGGKTVLVG 109
DB 213 FSGSSGNTGSLITLITGAQAEDEADYYCGSRDSSGCIHVFGGKTVLVG 261

RESULT 2
US-09-260-527-1
; Sequence 1, Application US/09260527A
; Patent No. 6228599
; GENERAL INFORMATION:
; APPLICANT: Knox, J.P.
; APPLICANT: Mikkelson, J.D.
; APPLICANT: Willats, W.G.
; TITLE OF INVENTION: ANTIBODY
; FILE REFERENCE: DYOUI9.001AUS
; CURRENT APPLICATION NUMBER: US/09/260,527A

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CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 280
TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
OTHER INFORMATION: phage display library known as the synthetic scfv
OTHER INFORMATION: library (#1) from the Centre for Protein
OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
US-09-260-527-1

Query Match 90.8%; Score 525; DB 4; Length 280;
Best Local Similarity 91.7%; Pred. No. 7.7e-44;
Matches 100; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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OY 61 FSGSGSGNTGSLITGGAQAEDEADYYCGSRDSSGIHVFGGKTLYVLG 109
|||
Db 215 FSGSSSGNTASLITGGAQAEDEADYYCNSRDSSGNHVFGGKTLYVLG 263

RESULT 3
US-09-079-029-9
Sequence 9, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapal, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-9

Query Match 90.8%; Score 525; DB 4; Length 309;
Best Local Similarity 91.7%; Pred. No. 8.6e-44;
Matches 100; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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OY 61 FSGSGSGNTGSLITGGAQAEDEADYYCGSRDSSGIHVFGGKTLYVLG 109
|||
Db 235 FSGSSSGNTASLITGGAQAEDEADYYCNSRDSSGNHVFGGKTLYVLG 283

RESULT 4
US-09-079-029-10
Sequence 10, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapal, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-10

Query Match 90.8%; Score 525; DB 4; Length 312;
Best Local Similarity 91.7%; Pred. No. 8.7e-44;
Matches 100; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 SSETLQDPAVSVAGQVTRITCGDLSLRFHPNMYQOKPGAPVLYTGKNNRPSGIPDR 60
|||
Db 178 SSETLQDPAVSVAGQVTRITCGDLSLRFHPNMYQOKPGAPVLYTGKNNRPSGIPDR 237
OY 61 FSGSGSGNTGSLITGGAQAEDEADYYCGSRDSSGIHVFGGKTLYVLG 109
|||
Db 238 FSGSSSGNTASLITGGAQAEDEADYYCNSRDSSGNHVFGGKTLYVLG 286

RESULT 5
US-08-652-816A-16
Sequence 16, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG